79	6	26 212	46 272	932 332	392	106 452	126 512	146 572
SAGTC	A GCG	C TGC	C TGT	CII	Y TAC	N AAT	, G G G	Q CAG
	P CCT	H CAT	C TGC	F	M ATG	P CCA	P CCG	P
36660	Q CAG	K AAG	D GAC	W	R CGC	P	GGA	S TCA
gaed	R CGC	K AAA	E GAG	FTTC	R AGG	Q CAG	G GGA	N AAC
ာဘား	R AGG	A GCC	YTAC	Y TAC	R CGG	R AGG	P CCA	CCC
ಶಿವಿಧಿತ್ಯ	M ATG	E GAA	S	W TGG	I ATC	T ACC	D GAC	P CCA
ಶಿವಿಧಿನ	2251	T ACA	R CGC	L CTG	F TTC.	Y TAC	TACT	V GTC
STCIG	BAGGA	C TGC	C TGC	R AGG	FTTC	S TCC	Y TAC	Q CAG
GCAG	GCGCGCTGGAGGACGCGAGGAGCC	E GAG	I ATA	Q CAG	9 660	V GTG	$f Y \\ TAT$	H H H H C
3GGC1		L TTG	Y TAT	I ATA	A GCC	N AAT	P CCC	A GCT
CICC		CHC	Y TAT	S	G GGA	FTC	P CCG	M ATG
\CGG(L CTG	ACC	CHC	C	A GCC	666	A GCA
	36600	GGG	P CCA	A GCC	C TGC	P CCA	P CCG	M ATG
CGTO	TCC	CHC	Y TAT	0 0 0 0	FTTC	EGAG	Q CAG	S
SGACC	22552	CIG	LCTC	V GTG	CTT	E GAG	Q CAG	N AAT
GTCGACCCACGCGTCCGCGGACGCGTGG	BACCC	L	G GGA	C	V GTG	I ATC	A GCC	999
	TGCG	A GCG	E GAA	C FGC	9 660	$_{ m CTG}$	G GGA	V GTC
	၁၁၅၁၅	A GCG	H H H C	R AGG	M ATG	P	P CCA	PCCT
GACC	GCGAAGCGCCCTGCGACCCGGCGTCCGG	∨ GTG	Y TAT	S TCC	M ATG	P	9 66C	N AAC
GTC	<i>1</i> 525	K AAG	A & G	9 990 900	LCTG	P	CCC	M ATG

Fig. 1A

BEST AVAILABLE CC

DOTERNAL OFFICE

166	632	173	653
ĿЭ	GAA		
X	TAC		
Д	SCG		
Ы	$\mathcal{C}\mathcal{C}\mathcal{C}$		
Ы	SCG		
ы	CCT		
⊱⊣	ACG		
Z	AAC		
C	IGC		
×	TAC		
Ø	225		
Ы	CCA		
Д	CCI		
Д	\mathcal{CCC}	*	TAG
Д	೮೦೦	ᄶ	AAG
A C P	IGC	A	CCC
A	೨೨೨	ᄶ	AAG
S	GTG	>	GTG
	AGT	>	GTA
ŋ	366	Ø	CAG

1206 1996 696 1285 1443 890 1048 1127 1364 1522 1601 1680 1759 1838 1917 IGTGTGAACGCTGACCTGTCCTGTGTGCTAAGAGCTATGCAGCTTAGCTGAGGCCGCCTAGATTACTAGATGTGCTGTAT CACGGGGAATGAGGTGGGGGGTGCTTATTTTAATGAACTAATCAGAGCCTCTTGAGAAATTGTTACTCATTGAACTGG AGCATCAAGACATCTCATGGAAGTGGATACGGAGTGATTTGGTGTCCATGCTTTTCACTCTGAGGACATTTAATCGGAG TGGGGTGCCCACGTGCAAGAGAGAGACAGGAGAGAGGCCTTTCCCTGGCCTTTCTGTTCTGTTGATGTTCACTTCCAG IGCTGGAGGTGCAGGTGGCATGTAGAGGGGCCAGGCCGAGCATCCCAGGCAAGCATCCTTCTGCCCGGGTATTAATAGG CTGTTCATATCCTAAAGATAGACTTCTCCTGCACCGCCAGGGAAGGGTAGCACGTGCAGCTCTCACCGCAGGATGGGGC CTICCIGCCCCAAACTGAGACATTGCATTTTGTGAGCTCTTGGTCTGATTTGGAGAAAGGACTGTTACCCATTTTTTG CICTCCAGGGCATICTCAGGCCCCGGGGGTCTCCTTCCCTCAGGCAGCTCCAGTGGTGGGTTCTGAAGGGTGCTTTCAAA STIGGGICTAAGCGGGIGIGIGCIGGCCICCAAGGAGGAGGAGCTIGCIGGGAAAAAAAAGACAGGAGAAGIACIGACICAAC TGCACTGACCATGTTGTCATAATTAGAATAAAGAAGTGGTCGGAAATGCACATTCCTGGATAGGAATCACAGCTCA <u> AGTACAATATATGAACTCACACTTTGTCTCCTCTGTTGCTTCTGTTTCTGACGCAGTCTGTGCTCTCACATGGTAGTGT</u>



2470 2549 2865 2628 2707 AACCTCCTGGGGAATTTTGTGGGAGACACTTGGGAACAAAAACAGACCCTGGGAATGCAGTTGCAAGCACAGATGCTG CCACCAGIGICICIGACCACCCIGGIGIGACIGCIGACIGCCAGCGIGGIACCICCCAIGCIGCAGGCCICCAICIAAA TGAGACAACAAGCACAATGTTCACTGTTTACAACCAAGACAACTGCGTGGGTCCAAACACTCCTCTTCCTCCAGGTCA TTTGTTTTGCATTTTTAATGTCTTTATTTTTTGTAATGAAAAGCACACTAAGCTGCCCCTGGAATCGGGTGCAGCTGA TTGTGCCCACTTCCTGGAGTGAGACAGCTCCTGGTGTGTAGAATTCCCGGAGCGTCCGTGGTTCAGAGTAAACTTGAAG ATAGGCACCCAAAAGTCCGTGACTAAATTTCGTTTTGTCTTTTTGATAGCAAATTATGTTAAGAGACAGTGATGGCTAGG AAAAAAAAAGGGGGGCGGC

Fig. 1C

GCGGACTGGCCCTGAGCTGGCCGTACAGCCCGGCTTCGGACGGTCCTCGCTGGAGCC ATG GGC CGC CGG CTC

G R V A A L L G L L V E C T E A K K H GGC AGG GTG GCG CTG CTG CTG CTA GTG GAG TGC ACT GAG GCC AAA AAA CAT

Fig. 1D

norman nataona

45	65 331	85 391	105 451	125 511	145 571	165 631	173 655
C TGC	F	M ATG	PCCA	PCCC	PCCT	Y TAT	
D GAC	W TGG	R CGC	P CCA	G GGA	S TCA	CCC	
E GAA	F TTT	R CGG	Q CAG	G GGA	N AAT	PCCC	
Y TAT	Y TAT	R CGC	R AGG	CCT	CCC CCC	P CCA	
S	W TGG	I ATT	T ACC	D GAC	Q CAG	CCT	
RCGT	L	F	Y TAT	T ACC	V GTC	T ACG	
C TGC	R AGG	F TTC	S	Y TAC	Q CAG	N AAC	
I ATA	Q CAG	GGT	V GTG	Y TAT	H H H C	C	
Y TAT	I ATA	A GCC	N AAT	P CCA	A GCT	Y TAC	
Y TAC	S	G	F TTC	P	M ATG	S	
T ACA	L	C TGT	T ACA	G GGA	A GCT	PCCT	
P	A GCC	C TGC	CCC	M ATG	M ATG	PCCT	
Y TAT	R AGG	F	E GAG	Q CAA	TACC	P CCC	* TAG
L	V GTG	L	E GAG	Q CAG	N AAT	P CCA	K AAG
GGA	C TGT	V GTG	I ATT	A GCA	0 9	Y TAC	D GAC
E GAA	C TGC	GGT	L	G GGA	V GTT	T ACT	K AAG
FTT	R AGG	M ATG	P CCA	P CCA	PCCT	T ACA	V GTG
Y TAT	S TCC	M ATG	P CCA	A GCT	N AAT	9	V GTG
W TGG	9 66C	L	P	PCCT	M ATG	G GGA	Q CAG
C TGC	$_{ m TGT}$	L	$\mathbf{Y}\\\mathbf{TAT}$	N AAT	GGG	H CAC	E

lig. 1E

CAAGATGCTACATCAAAGGCAAAGGGATGGACAGGCCCTTTTTGTTTACCTTCCCATCCTCACCGATACTTGCTGATAG 734

1840 1919 2156 2393 2472 1366 1603 1682 1998 2235 2314 1445 1761 2077 1208 1287 152 ATGGAAATTGCACTTCTGGGTATATGTCCCAGCATCCTTGTTTTCTTATGTTTGGTGAGTAAGGCTCACCCCTTCCAGC CATGACTAAATCTTATCTTTTGATAGCAAATCCTTTTAAGAAACTGAACAATTGCTAAGGCTCAGCAATTTTATACTC CAATGICIGIGIAAGGIAAAITITIGITIGCCATIGAGCCCACAITGGAAITCCITCIGACGICAACACIGACAAIGCCI GAAGAGGGGACGTTTGTGGATAGAGCCGTGAAAACCTACTTAGTTGCACAGATGACATAATCAAAAGTAGAGAAGAAG GAGTATICTTTACCACCTACAAGACCAGGAGGCATGGTGTCATTCTCCATTGGGGTATTTATATGAGGTAGAGGTTCAG GAATCGACAGTAGCTGTGTGGGCTTAGTTTAAGGACTGAAAGCATAGGGACTGGTAGACAGTTTCATAGGAAACTGCGG GGAAGGAATGGATACCTTTAAAGACAGTTTGTGGATGCAGATGCTGCCACCCATCATTGAGCACCCTTGTGTCTCTGGGC TTCCTGTCACTGGATCCAGTACCCCTCCATGCTTGGGTCCTTGTTTTACATAAGACAACAAAGCACAATGTCTGCTGTT TACAATCAAGACGACTACATGGTCCAAACATTTCTTCTCTTTTTTTCACTTGTGGCTTTAACTTCCATTTCCTCCGTT CCTTTTTAAAATCAAGAAGCACAGTCAGAGCTGCCCCTGGGATTGCATCAGGGAACGGCTGATCAAGGCATTCAGTGTC TCCCAGCCCATTCTCCTAATAGAAGCTGTGGGGCTGTGTTGTTGATGCTCTTTGGTCTCCACTCACATTTTGAAAATAG GCTTTCCTCTGCAGGAATAGGAAAAGACCCAAGTACATATTTGCTTCCACTTAAAAATGAGGGTCAGAACCAGGCCTCAG GCGTTTTATGAATCATCGTCTGGCTTTTTTTTAGTGCATGTATTGAAGTGAGGGTGTCCTTTGAGATCAGATGGGGAG TTATGGGCACTATAGAGCTGAGGGGCACATTAGGCCGGGTAGTTACATTGACCCTTGGAGAGGAAGAGGGACAGCCAAAG AAACTCAGCAAAGCAAGACCAGCATTGCTGAGTTAGAGCTAGGGTTGTATGTGATCCCCAACAGAGATGTGCTGGCCTCA TGTAGTTAGAGATGCCATTTCCCCAGGTGAGAATCAGAGCTCATCCATAGATTTACAAGTAGTGGCTGGAGTTAAACAGTA TGGAGTTCTTTTCCCTTGCGTAGTTAGTCACGTTGATGTGTATTTAAACCCCAGGTTGAGACCTTGTGTACTAAGAGCAA TAAATGAGAAAATCAGAGCCATTTGATAAACTGTTACTTGTTGGATCAGGCATCCAAAAGTGTCTTTGAGTGGACATT GGTGGTCCAAGGGAAAACTTGGATATTCTCAAAGCAAGCCCAGCTCTTTTCAAGTCTTTTGTGGAGGACATTTGAATC CAGATAAAGTGGTCAGGCTGAGATAAGACTCACATGATGCAGTAGTTGGCAGTGAACTTCGAAGAGAGACACTATCCACCA TTGGACATCTATAGTTAAATAAGGCCATTAGAGGGGGAAATCTTTAAGTTAGGGGAAATTCTCTAAATGGAGACATT AGTGAACTCTGCGGGGGGTGGGGTGTCTCTACTCAGAGGGCTCCAACACCCTTTTTCTTAGGTAGTTCTGGTGATGGGTT

Fig. 1F

DEPENDIA DIAGRA

2867 2788 2915 AGCTCTACTICTGTGTGCTGAGGTCCTGTAGAGCCGGGGCTTGGGCCACAGACATGAGGCCAGACTTGTGCATGCTCTTTC TIGGCAACACTIGGCTCATATITCTTGTTCTCTTTTGATAGAGTCCTGTTTCCTATGTATTAAAAATAAAAGTG

Fig. 1G

MRRQPAKVAALLLGLLLECTEAKKHCWYFEGLYPTYYICRSYEDCCGSRCCVRALSIQRLWYFWFLLMMG ::::::::::::::::::::::::::::::::::	80 100 110 120 130 140 VLFCCGAGFFIRRRMYPPPLIEEPAFNVSYTRQPPNPGPGAQQPGPPYYTDPGGPGMNPVGNSMAMAFQV ::::::::::::::::::::::::::::::::::::	150 160 170 PPNSPQGSVACPPPPAYCNTPPPPYEQVVKAK .::::::::::::::::::::::::::::::::::
20 LLLECTEAKKHCWYF: :::::::::::::::::::::::::::::::::::	90 10 MYPPPLIEEPAFNVS::::::::::::::::::::::::::::::::::::	160 PAYCNTPPPPYEQVV) :.:::::::::: PSYCNTPPPPYEQVV] 160
10 MRRQPAKVAALLLGLLLEC : :::::::::::::::::::::::::::::::::::	80 7LFCCGAGFFIRRRMYPPI 1:::::::::::::::::::::::::::::::::::	150 PPNSPQGSVACPPPPAYCN::::::::::::::::::::::::::::::::::::
Hum. MRRQ] : :. Mur. MGRR]	Hum. VLFC(:::: Mur. VLFC	Hum. PPNS] .::: Mur. QPNS]

Fig. 1H

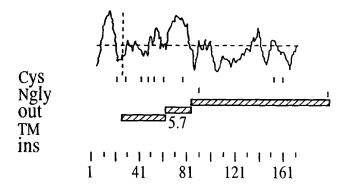


Fig. II

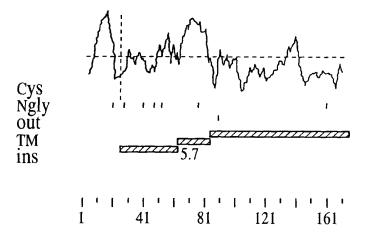


Fig. 1J

79	152	26 212	46	66 332	86 392	106 452	126 512
ATA	F TTT	H CAC	C TGC	Y TAT	L	Q CAA	G GGA
AATA	Q CAG	CIC	N AAC	Γ	S	V GTT	P CCT
TLGL	L TTA	L TTA	I ATT	T T T	H CAT	FTT	D GAT
TGAG	GGA	L TTA	Q CAA	V GTT		A GCC	$_{ m L}$
CAGC	C TGT	L TTA	R AGA	T ACA	G GGA	K AAA	R CGC
GAAT	M ATG	CII	G GGG	S AGT	T ACA	P CCA	K AAA
CTTCAGATTTAAAAAGAAACCTTTACTGAATCAGCTGAGTGTTAATAATA		Y TAT	T ACT	E GAA	L TTA	Y TAT	I ATC
	CAGG	C TGT	C TGC	PCCT	E GAA	V GTA	F TTC
	AGAA	T ACC	L	F TTT	S AGT	Y TAT	N AAT
AAAG	TCCA	V GTT	Q CAG	N AAT	E GAA	L CTG	N AAT
TTAA	AAAA	V GTT	C TGT	K AAG	N AAT	I ATT	N AAT
AGAT	ACAG	L CTG	V GTT	P CCT	I ATA	N AAC	$_{ m CTA}$
CTTC	CTGA	H H H H	s TCT	I ATT	$^{ m Y}$	S TCT	F TTT
CGTI	TGAT	L CTG	S TCG	S AGT	s TCT	N AAT	$_{ m CTA}$
ATGI	ATTC	R CGA	C TGT	S TCG	I ATA	D GAT	F TTT
GTCGACCCACGCGTCCGGAAATGTCGTT	GCCA	L CTA	G GGA	CTT	N AAT	$rac{ ext{L}}{ ext{TTG}}$	Y TAT
	TCTI	C TGC	L	9	N AAT	Y TAT	L CTA
	CTTI	P CCT	I ATA	L TTA	GGG	L TTG	H CAT
ACCC	CGAATTTCCTTTCTTGCCAATTCTGATCTGAACAGAAAATCCAAGAACAGGGAT	L CTG	E GAA	N AAC	T ACT	A GCA	R AGG
GTCG	CGAA	S TCT	K AAA	R CGT	L CTG	V GTA	$_{ m L}$

Fig. 2A

146	166	186	206	226	246	266	286
572	632	692	752	812	872	932	992
FTTT	N AAT	D GAT	CIT	V GTA	F TTT	N AAT	N AAT
S TCT	R AGG	L	N AAC	E GAA	P	R AGG	H CAT
V	Q	I	E	F	Q	I	S
GTA	CAA	ATA	GAA	TTT	CAG	ATT	AGT
Q CAG	L CTA	R CGG	L	A GCC	I ATA	R AGA	$_{ m L}$
N	N	L	H	N	A	S	I
AAT	AAT		CAT	AAT	GCA	TCA	ATC
Y	L	A	Q	S	E	N	$rac{ ext{L}}{ ext{TTG}}$
TAT	TTA	GCT	CAA	TCA	GAA	AAT	
Q	Y	V	F	P	I	K	H
CAG	TAC	GTT	TTT	CCA	ATT	AAA	CAT
L TTA	Q CAG	M ATG	S G G G	V GTA	P CCT	$_{ m CTG}$	K AAA
Y TAT	V GTT	G	S TCA	K AAA	N AAT	L	L
L	S	V	E	T	H	L	N
TTA	TCA	GTT	GAA	ACA	CAT	CTC	AAT
N	V	F	S	L	SHICH	Y	N
AAT	GTT	TTT	TCA	TTA		TAC	AAT
R	L	T	I	N	L	E	I
CGT	CTA	ACC	ATA	AAT	TTG	GAA	ATT
L	D GAT	GGT	R AGG	N AAT	S TCT	L CIG	G GGA
N	N	S	L	S	CTT	N	S
AAT	AAT	AGT	TTG	AGT		AAT	AGT
$_{ m LTA}$	F T T T	GGG	I ATT	G GGA	R AGA	A GCC	F TTT
L	V GTA	L CTT	N AAC	L TTA	R AGA	L	GGG
G GGA	G GGA	V GTC	N AAT	Y TAT	L	GGA	D GAT
K	R	T	N	$_{ m ITG}$	S	K	R
AAG	AGA	ACT	AAC		AGT	AAA	AGG
F	P	L	S TCA	$_{\rm TGT}^{\rm C}$	K AAA	F TTT	T ACT
I	V	R	L	A	L	A	V
ATA	GTT	CGC	TTA	GCT		GCA	GTT

Fig. 2B

346 1172 386 1292 366 1232 426 406 352 446 K AAA Q CAG T ACA K AAG N AAT K AAG S TCT E GAA $_{\rm TGT}^{\rm C}$ H CAC CTT C TGC V GTT A GCA LCIT N AAC Y TAT H CAT L CTG $^{
m Y}$ GGA V GTC $_{\rm TGT}^{\rm C}$ M ATG I ATC N AAT I ATT R AGG $_{\mathrm{TGT}}^{\mathrm{C}}$ I ATT PCCT N AAC T ACA H CAT L TTA N AAT P CCA E GAA S AGT I ATT N AAT E GAA $\overline{\mathbf{W}}$ L CTA PCCT 9 660 H CAT N AAC K AAG $_{
m L}$ T ACT S TCT N AAT FTTT PCCT T ACA I ATT I ATT K AAA L TTA T ACA A GCC N AAT T ACC S TCT A GCC Y TAT VGTA $_{
m L}^{
m L}$ D GAT T ACA R CGT V GTT V GTA S TCA L CTT N AAT N AAT AGT S K AAA A GCA L TTA TIC D GAT N AAT S TCT A GCT W TGG H CAT ACA N AAT Q CAG A GCA GCA Ø L CTA R AGA A GCT $\overline{\mathbf{W}}$ GAC L S AGC F TTT Ω R AGA A GCC $\overline{\mathbf{W}}$ GGC S TCT I ATT S TCA H CAT L CTG M ATG S TCC I ATA I ATT D GAC R CGT AAT \mathbb{Z} M ATG R AGA $_{\rm ITG}^{\rm L}$ R CGA M ATG V GTA L TTA N AAT L N AAT S TCC AAT N AAC LCTT S TCA CIT Z A GCG I ATA GGC E GAG R AGA I ATC S TCT P CCA TACT K AAG $_{
m L}$ L TTG P TCA L TTA D GAT ഗ S TCT T ACT $_{
m L}$ P N AAT L D GAT L TTA

Fig. 20

TOPECTA CAROLI

466 1532	486 1592	506 1652	526 1712	546 1772	566 1832	586 1892	606 1952
FTT	I ATA	A GCT	E GAG	I ATC	R AGA	N AAC	I ATT
R AGA	Q CAA	D GAT	N AAT	$rac{ ext{L}}{ ext{TTG}}$	N AAT	$^{\mathrm{C}}$	Q CAA
GGT	V GTG	N AAT	$_{ m L}$	${ m F}$	E GAA	I ATT	K AAA
A GCT	P CCT	P CCG	K AAG	I ATT	R AGG	S TCA	H CAT
PCCT	L TTA	L CTA	E GAG	I ATC	S TCA	A GCC	L CTT
S TCA	V GTG	A GCT	V GTT	$_{ m LTA}$	N AAC	TACT	R CGA
T ACT	A GCA	S AGT	E GAA	V GTT	E GAA	V GTA	I ATT
P CCT	TACA	N AAC	CAA	$_{\rm TGT}^{\rm C}$	S TCA	N AAT	Q CAG
I ATT	TACT	K AAA	T ACA	A GCT	A GCA	Y TAT	E GAG
R CGA	E GAG	E GAA	$^{ m C}_{ m TGT}$	$_{ m L}$	K AAG	R AGG	Γ
E GAA	L TTA	$_{ m L}$	I ATT	I ATC	L CTA	A GCA	GGC
W TGG	P CCA	N AAC	$_{ m CTA}$	F	K AAA	S TCA	P
FTTC	N AAT	$rac{ ext{L}}{ ext{TTG}}$	S TCT	F TTT	Q CAA	Q CAG	S AGT
TACT	GGT	T ACC	T ACA	A GCT	K AAA	Y TAT	E GAA
I ATT	F TTT	V GTT	K AAA	L CTA	F TTT	F TTT	L CTA
N AAC	A GCC	S TCT	999	Γ	Q CAG	S AGC	S TCT
E GAG	N AAT	T ACT	S TCA	I ATT	V GTT	$^{ m Y}$	N AAT
TACT	E GAG	T ACT	M ATG	D GAC	V GTT	$^{ m Y}_{ m TAC}$	P CCA
E GAG	OCAA	Γ	S TCA	F TTT	K AAA	E GAA	S TCC
TACT	F TTT	Q CAA	A GCT	A GCT	Y TAC	L	T ACT

Fig. 2D

623 2003	2082	2161	2169
V I L F E H S A L \star 623 GTC ATT CTT TTT GAA CAT TCT GCT TTA TAA 2003	ctcaactaaatattgtctataagaaacttcagtgccatggacatgatttaaactgaaacctccttatatata	tttagttggaaatataatgaattatgaggttagcattattaaaaatatgtttattaaaaaaaa	2169
	CTTCA	TGAGG	
CA	AAA	ATA	
A GCA	'AAG	ATT	
V P E N E A Q GTT CCT GAA AAT GAG GCA CAG	rctai	AATGA	
N AAT	ATTG	ATATA	
E GAA	AAAT	3GAAJ	()
PCCT	AACT	4GTT(ວອວວອອວອ
V GTT	CIC	TTT	909

Fig. 2E

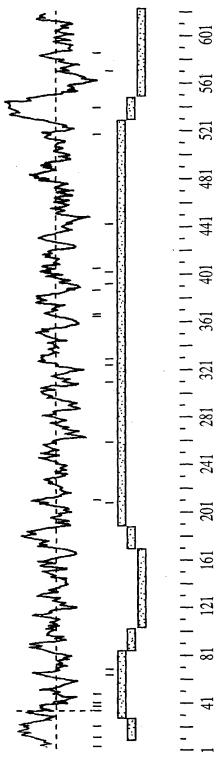


FIG. 2F

Selys Selys Transins

COZEELL CLISSI

Fig. 20

DOVESELL LOLLOCL

280 330 340 Slit AACTCSNNIVDCRGKGLTEIPTNLPETITEIRLEQNTIKVIPPGAFSPYKKLRRIDLSNNQISELAPDAF ::::::: 325LRILDLSNNNI	350 360 410 QGLRSLNSLVLYGNKITELPKSLFEGLFSLQLLLLLNANKINCLRVDAFQDLHNLNLLSLYDNKLQTIAKG :: :: :: :: ::	420 430 440 450 460 470 480 TFSPLRAIQTMHLAQNPFICDCHLKWLADYLHTNPIETSGARCTSPRRLANKRIGQIKSKKFRCSAKEQY :::: 210	00 510 520 530 540 550 CFADLACPEKCRCEGTTVDCSNQKLNKIPEHIPQYTAELRLNNNEFTVLEATGIF .:.: .220
310 EIRLEQNTIKVIPPGAFS	380 390 LQLLLLNANKINCLRVDA	450 460 DYLHTNPIETSGARCTSPI :: .: -YLGSN	520 530 GTTVDCSNQKLNKIPEH: .:.:: NLTKVP
290 300 RGKGLTEIPTNLPETIT	360 370 GNKITELPKSLFEGLFS :::	430 440 ILAQNPFICDCHLKWLADY: :	500 510 SGDCFADLACPEKCRCE
280 Slit AACTCSNNIVDC 325	350 Slit QGLRSLNSLVLN :: 325LR	420 Slit TFSPLRAIQTMI 325	490 50 Slit FIPGTEDYRSKLSGD 325

Fig. 2H

nozekul ellen

0 580 610 620 ITDIEEGAFEGASGVNEILLTSNRLENVQHKMFKGLESLKTLMLRSNRITCVGND : .: .: .: .: .: .: .: .: .: .: .: .: .:	630 640 650 670 680 690 SFIGLSSVRLLSLYDNQITTVAPGAFDTLHSLSTLNLLANPFNCNCYLAWLGEWLRKKRIVTGNPRCQKP :::::::::::::::::::::::::::::::::	700 710 720 730 740 750 760 YFLKEIPIQDVAIQDFTCDDGNDDNSCSPLSRCPTECTCLDTVVRCSNKGLKVLPKGIPRDVTELYLDGN :	770 780 800 810 820 830 QFTLVPKELSNYKHLTLIDLSNNRISTLSNQSFSNM-TQLLTLILSYNRLRCIPPRTFDGLKSLRLLSLH ::::::::::::::::::::::::::::::::::
580 590 FEGASGVNEILLTSNRLEN::	650 660 GAFDTLHSLSTLNLLANPI ::: LEN-	720 DNSCSPLSRCPTECTCLD'	790 800 RISTLSNQSFSNM-TQLL':::::::::::::::::::::::::::::::::::
560 570 58 LPQLRKINFSNNKITDIEEGAFE ::::::::::::::::::::::::::::::::::::	630 640 (SFIGLSSVRLLSLYDNQITTVAPC :::: GFSGINNLKHLILSHND280	0 IPIQDVAIQDFTCDDGNDI	0 780 PKELSNYKHLTLIDLSNNE ::: ::::::::::::::::::::::::::::::::
560 570 Slit KKLPQLRKINFSNNK:::325LRRLSLSHNP:230 240	630 Slit SFIGLS: .: : 325 GFSGINI	700 Slit YFLKEI 325	770 Slit QFTLVPK :.:. 325 TFSLL

Fig. 21

DOVECT CLICA

			r	
900 OKLLLTTPSK	970 NPCKHGGTCH :: -PSMRG	1040 EEKLDFCAQD	1110 EGYSGLFCEF	
890 ARCAGPGEMAI	960 DCDVPIHACISI : : : -CQNP	1030 CPPEYTGELCI	1100 AVNGYTCICP	TSSIN410
880 7KSEYKEPGI <i>F</i> . :	950 ICPYGFKGQDC	1020 JDGINNYTCLG:	1090 KCKNGAHCTD)	ST
50 860 870 SALSHLAIGANPLYCDCNMQWLSDWVKS::::::::::::::::::::::::::::::::::::	940 NSDPVDFYRCT : Y	1010 DNDCENNSTCVD : .:: NITNCV-	1080 DIDFDDCQDNI	
860 HLAIGANPLYCI :: .:: : HLQANSNPWECI 360	930 SNPCKNDGTC	1000 NCEVNVDDCE	1070 CTPGYVGEHC	
850 FNDLSALSH :::: SSLIH 350	920 ILAKCNPCL : I	990 ICADGFEGE : I	1060 LTPKGFKCL	
840 850 900 Slit GNDISVVPEGAFNDLSALSHLAIGANPLYCDCNMQWLSDWVKSEYKEPGIARCAGPGEMADKLLTTPSK ::::::::::::::::::::::::::::::::::::	910 920 930 940 950 960 970 KFTCQGPVDVNILAKCNPCLSNPCKNDGTCNSDPVDFYRCTCPYGFKGQDCDVPIHACISNPCKHGGTCH :::::::::::::::::::::::::::::::::	980 990 1000 1010 1020 1030 1040 LKEGEEDGFWCICADGFEGENCEVNVDDCEDNDCENNSTCVDGINNYTCLCPPEYTGELCEEKLDFCAQD:RALRYI	1050 1060 1070 1080 1090 1100 1110 LNPCQHDSKCILTPKGFKCDCTPGYVGEHCDIDFDDCQDNKCKNGAHCTDAVNGYTCICPEGYSGLFCEF	
Slit (slit 325	Slit 325	Slit	325

Fig. 2.

DOPERST Offor

1120 1130 1140 1150 1160 1170 1180 it SPPMVLPRTSPCDNFDCQNGAQCIVRINEPICQCLPGYQGEKCEKLVSVNFINKESYLQIPSAKVRPQTN:::::::::::::::::::::::::::::::::	1190 1200 1210 1220 1230 1240 1250 it ITLQIATDEDSGILLYKGDKDHIAVELYRGRVRASYDTGSHPASAIYSVETINDGNFHIVELLALDQSLS :::::::::::::::::::::::::::::::::::	1260 1270 1280 1290 1300 1310 1320 lit LSVDGGNPKIITNLSKQSTLNFDSPLYVGGMPGKSNVASLRQAPGQNGTSFHGCIRNLYINSELQDFQKV :: ::::::::::::::::::::::::::::::::::	1330 1340 1350 1360 1370 1380 1390 it PMQTGILPGCEPCHKKVCAHGTCQPSSQAGFTCECQEGWMGPLCDQRTNDPCLGNKCVHGTCLPINAFSY
slit 325	Slit 325	Slit 325 49	Slit 325

Fig. 2K

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1460	Slit SCKCLEGHGGVLCDEEEDLFNPCQAIKCKHGKCRLSGLGQPYCECSSGYTGDSCDREISCRGERIRDYYQ	: .::: RENRL-EYY-	570		GCTRCVS	•	-LFEHSAL	620
1450	GDSCDREISC	· · · : · · · · · · · · · · · · · · · ·	560	1520	VDEVEKVVK	•••	QIVPENEAQVI-LFEHSAL	610
1440	PYCECSSGYT	. 07	56	1510	SFECTDGSSE	•	 	
1430	SKCRLSGLGQ	.: . KIKA		1500	3PLRSKRRKY	••••••	SLEQIRLHK-	009
1420	PCQAIKCKHO	.: :	550	1490	GGCAGGQCC		ITSPNSLESP(590
1410	LCDEEEDLFN	Ļ		1480	K-KVSRLECR	•	RYNVTASICN	580
1400	CKCLEGHGGV	 	540	1470	Slit KQQGYAACQTTK-KVSRLECRGGCAGGQCCGPLRSKRRKYSFECTDGSSFVDEVEKVVKCGCTRCVS	•	325SFYQSARYNVTASICNTSPNSLESPGLEQIRLHK	
	Slit 8	325 AC			Slit		325 -	

Fig. 21

DOVEMBLA DILLOLI

70 ATT	 140 GGT) 0	
ATATT	IGCGC	 ,		GGCACCG ::: ACC-
10 20 30 40 50 50 70 Slit cagagcaggaggaggaggaggaggaggaggaggaggagga		325	270	GGCGTTGGCTGGCAGATGCTGTCCCTGTCGCTGGGGTTAGTGCTGGCGATCCTGAACAAGGTGGCACCGC :::
GCCTI		00550) } } }	TGAAC
50 ICTACI	120 120	190 190	09%	GATCC
TGGGC		3AGGAZ		3CTGGC
40 CTGAG	110	180	250	TTAGT
TGTGC	CTAGC	CAGTG		TGGGG
30 SAGGCG	100 3GGTTG	170 AGCCCC	240	rercec-
GGTGG				STCCC
20 AGGGC	90 CTGGC	 160 AGCTAN	5 I S	ATGCT
) GTGGAG	 TTTCC	CAGCA		GGCAG
10 3CAGGG	 80 3CACAT	150 150	220	TGGCT
CAGA(TCCCI		
Slit	325 Slit	325 Slit	325	Slit 325

Fig. 2M-1

DOYMELL LILODI

0 H	⊟	O 0 i	0 KJ !	Ö Ü Ü
350 AGCGT	:::	420 .CGAAG	490 TGAAA :. TA	560 TGTTTCC ::::
ລອລອ		ATTA	.ccarrg .:.::. ccrrra 50	.GCTG
340 GGCT		410 AAGA:	480 AGCA	550 TTCA
CTGG	1	TCAC	1GATT	TCACC .:. ACG
330 CACGG	:::: -CACG 10	400 ATAACA	0 460 470 AGTTCTTCAGCTTATGGAGAATAA ::::::::::::::::::::::::::	540 TTAAACAGAAATCAC ::::: :::: TTAATAATACG-
33 TGTCA	CZ	4(GAAA!	4. TGGAG; :. AAAAA(5, AACA(: AT
GGAC	 	AATG 	TTAT ::: TTTA	TTTA::::
320 CAGT		390 TTTA	460 CAGC' :::	530 TGCG
AGCA		TGGA	FTCTT::::	3AGAC : .: 3TG
290 340 350 Slit AGGCGTGCCCGGCGCAGTGCTCTGCTCGGGCAGCACAGTGGACTGTCACGGGCTGGCGCTGCGCAGCGT		360 370 380 420 GCCCAGGAATATCCCCCGCAACACCGAGAGACTGGATTTAAATGGAAATAACATCACAAGAATTACGAAG ::::::::::::::	430 440 450 460 470 480 490 Slit ACAGATTTTGCTGGTCTTAGACATCTAAGAGTTCTTCAGCTTATGGAGAATAAGATTAGCACCATTGAAA ::::::::::::::::::::::::::::::::	500 510 520 530 540 550 560 S11 Slit GAGGAGCATTCCAGGATCTTAAAGAACTAGAGACTGCGTTTAAACAGAAATCACCTTCAGCTGTTTCC
TGCT	 	CCGA	TCTA	5; .caacti
O SCTCT	 	70 YAACA	440 TAGACA	510 CTTAAA : C
300 SAGTGC	 	370 3CCGCA	44	51 CCAGGATCT ::::: -CTGAATC- 60
3606(ATCCC.	CTGG	CCAGG
290 GCCC		360 CCAGGAATA' :::::: CCGGAAATG' 20	430 TTTG	500 CATT
GCGT		360 CCCAGGAATATCC ::::::: -CCGGAAATGTC- 20	AGAT:	NGGAG
t AG	5		t AC 5	t GP
Sli	325	Slit 325	Slit 325	Slit 325

Fig. 2M-2

HOYEKTI DIIGI

630 GGCAATC :: GG	700 AGCTGTA ::GTT	770 TTACTAG	840 CCTGTAT :: AT 200
620 AAAACCAAATTCAG :::.::::::: AAATCCAAGAACAG 120	690 AACCAGATC : A	760 ATAACAACA : A	830 ITCAAACAA
580 620 630 630 630 630 630 630 630 630 TGGGACTGCGAAGCTATACAGGCTTGATCTCAGTGAAATCCAAATTCAGGCAATC ::::::::::::::::::::::::::::::::::	680 AACTGGATTAC. ::::::: TGGATTAC. 140	720 730 740 750 760 770 TCAGGGCTCTCCGGGACCTGGAAGTGCTCACTCTCAACATAACAACATTACTAG ::::::::::::::::::::::::::::::::::::	790 800 810 820 830 840 TTTCAACCATATGCCTAAACTTAGGACTTTTCGACTGCATTCAAACAACCTGTAT :: .:::. TTGTTACCTGTTATCTTTT
600 CAGGCTTGAT:::: CTGA	670 AAAAATTTGC. .:.: :: -GATATGTG-	740 3GAAGTGCT ::: TGC-	810 CTTAGGACTTTT .::::
590 CTGCGAAGCTATACAGG : ::: ::.::: CCAATTCTGATCTGA 100	660 TTGACATAA	730 CCGGGACCTG .:: GCCT- 160	800 ATGCCTAAA ::. TTA
580 TTGGGACTGCGA/ ::: :::: TTGC-CAA/		720 TTCAGGGCTCTC ::: CTCT-	
570 TGAGTTGCTGTTTCT::::: TTTTCT	640 CCAAGGAAAGCTTTC	710 TTGAAGATGGGGCAT :: TT	780 ACTTTCTGTGGCAAG :::: ::CTGTTTCTGG
Slit T : 325 T	Slit (Slit 7 325 7	Slit 7

Fig. 2M-

DOVERSIA STABOL

910 AGT :	980 TGG :::	1050 CAAT	1120 ATAC .:.:
9. CTCA(::	CAG:	10 AAC.	AAA'
ACAC	980 TCTGCAGTGG :::::::: TCTGCACTGG 250	4GC.	ACAG; :::: ACAG' 320
900 CTGTA(:::. -TGTT(230	970 TTGT(:	040 CTGT/ :: . CTTA(280	10 ICA(: : I-A(
90 3TCJ	9. ATT:	1040 GTACCTGTAGC ::: :: .:: GTAACTTAGGC 280	1110 CCATCZ
900 TTGGTCTGTACAC' :::: :::: TTGGA-TGTTCG-'	4GA7	rGTZ ::- -GTZ	1100 1110 112 ATCTTCCAGAGACCATCACAGAATA ::::::::::::::::::::::::::::::::::
GGG	ACG2		0 CAGAGA : . : . : CTGAAA
890 3TCG	960 4AAA(1030 GCCG(1100 TTCC/ TTCC/ TTCC/ 310
0 CAAAGGCC ::: .: -AAATAC- 220	ICA,	CC H	ATC: :: ATT
AAAG ::: AAAT. 220	GGT	20 ACTGCC ::::: ACTGCC 270	CAA
880 000 1	950 CGA	1020 GCACT ::: ACT	1090 CCCA(
H H C	AGCC ::: AGC-	TTG	1 1 1 - 1
) 1 1 1	TGT	GTT	80 CTGAGA ::.:: CTAAGA
870 GACT	930 940 950 960 970 980 ACCTGAGAGGCCATAATGTAGCCGAGGTTCAAAAACGAGAATTTGTCTGCAGTGG :::AGCAGC	1000 1010 1020 1030 1040 1050 GGCTCCTTCTTGTAGTGTTTTGCACTGCCCTGCCGCCTGTACCTGTAGCAACAAT ::::::::::::::::::::::::::::::::	1080 CACTGAGA:::::
8 5 5 1	9 1 1	10 TGT	10 CTCA
TCI	AGG	TLCI	0 AAGGTCT :: -TATTC-
	30 GAG	00 1001	70 4AAC T7
860 3CCTG	930 ACCTG	1000 3GCTC	1070 3GGAA:
TGG 	CTCCC? :: -TC	ratc : rta-	1 ACTGTCGTGG :: :::: -CTTTCGAG-
50 CCACC :::: CCACZ	CCTC	990 CCAGTCATTTAT :::::.:	60 CTGTCGT :: ::. CTTTCGA
850 FGCC ::: F-CC 210	920	990 AGTCA :::: AGACA 260	1060 GACT ::
SACT ::: FACT	TGG(:: TG	CCA(A(GTA(
850 TGTGACTGCCACCTG :.::::::: TATTACT-CCACAAA	920 GTATGGGCCCCTCCC ::.:: GTTTGTC 240	990 TCACCAGTCATTTAT :::::.: GAGACAAATTA	1060 1070 1080 1090 1100 1110 1120 ATCGTAGACTGTGGGAAAGGTCTCACTGAGATCCCCCACAAATCTTCCAGAGACCATCACAGAAATAC :::::::::::::::::::::::::::::::::
850 860 910 910 Slit TGTGACTGCCACCTGGCTCTCCGACTGGCTTCGCCAAAGGCCTCGGGTTGGTCTGTACACTCAGT ::::::::::::::::::::::::::::::::::::	Slit 325	Slit 325	Slit 325
S1 3	S1 3	S1 3	S G

Fig. 2M-

DOVEMENT DITTOPE

1130 1140 1150 1160 1170 1180 1190 Slit GTTTGGAACACAATCAAAGTCATCCTCCTGGAGCTTTCTCACCATATAAAAAGCTTAGACGAAT :::::::::::::::::::::::::::::::::::	1210 1220 1230 1240 1250 1260 TCAGATCTCTGAACTTCCAAGGACTACGCTCTCTGAATTCA :::::::::::::::::::::::::::::::::	1270 1280 1300 1310 1330 CTTGTCCTCTATGGAAATCACAGAACTCCCCCAAAAGTTTATTTGAAGGACTGTTTTCCTTACAGC ::::: CTTGTAGCAGCATTGTATTTGGATAATTCTAACA 400 410 420	1340 1350 1360 1370 1380 1400 TCCTATTATTGAATGCCAACAAGATAAACTGCCTTCGGGTAGATGCTTTTCAGGATCTCCACAACTTGAA ::::::::::::::::::::::::::::::::::
1170 118 TCTCACCATATAAAAA(: ::::::::::::::::::::::::::::::::	1240 TTTCCAAGGACTAC::::::::::::::::::::::::::	0 AGTTTATTTGAAGGACT : :::::: ATTGTATTTGGA	1380 SATGCTTTTCAGGAT : : : : :: ::TTCAATTGAGG450
1160 :::::::::::::::::::::::::::::::::::	1230 scaccagatgo	1300 CCCCAAAAGT : : ATT	0 1370 TGCCTTCGGGTAG ::::: :
1150 AAGTCATCCCI	1220 STCTGAACTTC	1290 ATCACAGAACT ::: AGC-	1360 AGATAAACTGCO ::
1140 AACACAATCAA	1210 ATAATCAGATC	1280 rggaaataa <i>ai</i>	1350 AATGCCAACAA(.::::::: IAT-CCAAAA-
1130 GTTTGGAACAGA ::::::: TGTATCTGA 330	1200 TGACCTGAGCAATAA :.:: TAAC	0	
Slit 325	slit 325	Slit 325 39	Slit

Fig. 2M-5

DATESTA DATEDA

1410 1420 1430 1440 1450 1460 1470 CCTTCTCTCCCTATATGACAACAAGCTTCAGACCATCGCCAAGGGGGACCTTTTCACCTCTTCGGGCCATT ::::::::::::::::::::::::::::::::::	1480 1490 1500 1510 1520 1530 1540 Slit CAAACTATGCATTTGGCCCAGCATTATTTTTGTGACTGCCATCTCAAGTGGCTAGCGGATTATCTCC ::::::::::::::::::::::::::::::	1550 1560 1570 1580 1590 1600 1610 ATACCAACCCGATTGAGACCAGTGGTGCCCGTTGCACCAGCCCCGCCGCCTGGCAAAAAAATTGG ::: GTAATTTATATTT 550	1620 1630 1640 1650 1660 1670 1680 Slit ACAGATCAAAAGCAAGAATTCCGTTGTTCAGCTAAAGAACAGTATTTCATTCCAGGTACAGAATTAT :::: :::::::::::::::::::::::::::
Slit CCTTCTC:::325 T-TTCTA	Slit CAAACTA ::::: 325 CAAAC	1 Slit ATACCAA ::: 325 GTA	Slit ACAGATC::::

Fig. 2M-6

DOVECETT OTTOOT

1750 3GAACCA	1820 AGTTGCG	1890 ACGTAAA	1960 STAAATG
1740 CGCTGTGAAG	1810 ACACTGCAG/ :::: -CACTG	1880 TTCCTCAATT::::: TACCT	1950 GCATCTGGT(:.::: -CTTCGG680
1730 :GAAAAGTGT	1800 ATTCCCCAGT:::TCGCCT	1870 FTAAGAAACT :	1940 ATTTGAAGGA
1720 GGCTTGCCC1 : .G	1790 CCGGAGCAC <i>I</i> ::: GGAA	1860 CAGGAATCT7 .:: -TGG	20 1930 ATATTGAGGAGGAGCAT ::::: .:: .:: TTGTTGGTATGGTTGCT- 670
1710 TTGCGGATCTG :::::::	1780 CAACAAAATC ::: CAAA	1850 TTGGAAGCCA :::::: TTGGGAG	1920 CAGATATTGA .::::.
1700 3GAGACTGCT	1770 AATCAAAAGCT: ::::: AATCTA	1840 ATTTACCGTG .:: TCC	1910 AATAAGATCA
1690 1700 1710 1720 1730 1740 1750 Slit CGATCAAAATTAAGTGGACTGCTTTGCGGATCTGGCTTGCCCTGAAAAGTGTCGCTGTGAAGGAACCA :::::::::::::::::::::::::::::	1760 1770 1780 1790 1810 1810 1820 CAGTAGATTGCTCTAATCAAAAGCTCAACAAAATCCCGGAGCACATTCCCCAGTACACTGCAGAGTTGCG :::::::::::::::::::::::::::::::::	1830 1840 1860 1890 1890 1890 1890 1890 1890 1890 189	1900 1910 1920 1930 1940 1950 1960 ATAAACTTTAGCAACAATAAGATCACAGATATTGAGGAGGAGCATCTGGTGTAAATG .:.::::::::::::::::::::::::::::::::
Slit G	Slit C 325 -	Slit T 325 -	Slit A 325 -

Fig. 2M-7

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30 AA 	о ^ტ ।	0 E I	0 H • H
2030 CTCAA :	2100 CTGTG	2170 FTCTT	2240 rggct
AGC	GTTC	CCAT	GAG
20 GGAA	90 CTCA	60 CTCT	30 GGGA : GTAT
2020 3ATTGG	2090 AGGACT	2160 3ATACT(2230 3GTTGG: :::: 3TTTGT,
AGG(CATA:::	TTT	2230 GCTTGGTTGGGA :::::::::: GCTTGTTTGTAT
2010 GTTCA	2070 2080 3GGGAATGACAGTTTC :	2150 :GGGC?	2220 CCTGG
2 GATG	2 TGACA ::: TATCA	2 CAGG	2 CTAC
) ATAA(SAATO	GCAC	ACTG
2000 AGCA'	2070 GGGG : ::	2140 GTTG	2210 GTAA
GTGC	GTGTC .: : ATTTJ	TACP	AACT
90 AAAT 	L I	2120 2130 2140 2150 2160 2170 TATGATAATCAAATTACTACAGTTGCACCAGGGGCATTTGATACTCTCCATTCTT	2180 2200 2210 2220 2240 TATCTACTCTAAACCTCTTGGCCAATCCTTTTAACTGTAACTGCTACCTGGCTTGGTTGG
1990 IGGAAA	2060 AATAAC :::::	2130 CAAATT	2200 CCAATCCTT' :::::::
GTT	TCG7	AAT(SCCAZ
1980 GTAATC ::::: TTTATC	2050 AGCAP	2120 ATGAT	2190 :rcrrgg ::::::
1 CGAGT :::: -GATT	2 AGAA		2 (CCTC : :: (CATC
) TTACG; : G; 690	STTG	CTT:::	0 TAAACC ::: AACA 74
1970 TTCT:	2040 GATG	2110 CGTTTGCTTTCTTTG ::::: GCTTTC	2180 ACTCT
19 AAATACTT :::::	.: .: .C	TTTG: : G	TCTF
•	2040 Slit AACTTTGATGTTGAG ::: 325 AAC700		
Slit 325	S11.	Slit 325	Slit 325

Fig. 2M-8

1975511 Ulland

2310 3CATC	2380 TTTCTC : ::: TGTCTC 840	2450 FTGCC ::::: FTGCC 890	2520 AGGAA
2300 TGAAAGAAATACC :::::: GAAGTAC-	2330 2340 2350 2360 2370 2380 CAGGACTTCACTTGTGATGACGAAATGATGACAATAGTTGCTCCCCCACTTTCTC ::::: AAAGTCTTAGAAGACTTTCTTTGTCTC 820	2400 2410 2420 2430 2440 2450 GTACTTGCTTGGATACAGTCGTCCGATGTAGCAACAAGGGTTTGAAGGTCTTGCC ::::::::::::::::::::::::::::::	2470 2480 2500 2510 2520 AGATGTCACAGAGTTGTATCTGGATGGAAACCAATTTACACTGGTTCCCAAGGAA :::::::::::::::::::::::::::::
2290 ACCATACTTCC :::: GCCTTT	2360 ATGATGACAATAG' .:.::.: -AGAAGACTTT	2430 STAGCAACAAG(::	2500 GGAAACCAATTTA(:::: ATACC
2280 22 SATGTCAAAAACCATA .::::.:::	2350 rgacggaaatg ::	410 2420 ATACAGTCGTCCGATG' ::::::::::::::::::::::::::::::::::::	2490 ATCTGGATGGAA ::::: -TCTGGAAT
0 2270 ACGGGAAATCCTA(:::: ACAAAAGTACC	2340 CACTTGTGA	2410 ITGGATACA(. :::: AATACA(2480 CAGAGTTGTA
2260 2270 TTGTCACGGGAAATCCT ::. :::: TTAACAAAAGTACC- 0 790	2330 ATTCAGGACTT(.:.:.:: TTAAAAGTCTT- 820		2470 GAGATGTCA(
2250 2260 2280 2290 2300 2310 Slit GAGAAAGAAGAATTGTCACGGGAAATCCTAGATGTCAAAAAACCATACTTCCTGAAAGAAA	2320 CAGGATGTGGCCATT	2390 GCTGTCCTACTGAAT : : : : : : : : : : : : : : : : :	2460 Slit GAAAGGTATTCCAAG .: 325 AA
Slit 325	Slit 325	Slit 325	Slit 325

Fig. 2M-9

2530 2540 2550 2550 2570 2580 2590 CTCTCCAACTACAACATTTAACATTATAGACTTAAGTAACAACAGAATAAGCACGCTTTCTAATCAGA :::::::::::::::::::::::::::::::	2600 2610 2620 2630 2640 2650 2660 GCAACATGACCCTCCTCCTCTTAATTCTTAGTTACAACCGTCTGAGATGTATTCCTCCTCG :::::::::::::::::::::::::::::	2670 2680 2700 2710 2720 2730 TTTGATGGATTAAAGTCTCTTCGATTACTTTCTCTACATGGAAATGACATTTCTGTTGTGCCTGAA ::::::::::::::::::::::::::::::::::	2740 2750 2760 2770 2780 2790 2800 GGTGCTTTCAATGCATTATCACATCTAGCAATTGGAGCCAACCCTCTTTACTGTGATTGTA :::::::::::::::::::::::::::::
2530 Slit CTCTCCAACTACAAA :::: ::325TCCTGAAAATT	2600 Slit GCTTCAGCAACATGA . :: : :.:.: 325 AATTAATAATCTTAA 960 970	2670 Slit CACCTTTGATGGATT :::::: 325TTTAGAGAATT	2740 Slit GGTGCTTTCAATGAT:::::::::325 GTTAGATAGAA

Fig. 2M-10

DOYGESTI DIIODI

2860 2870 cGTTGTGCTGGTCC : :::. ::: CTTTGAAGATCC 1120	2940 CTGTGGAT	3010 raatagig :	3080 CCAATICA :::: ATICA 1190
2860 GCTCGTTGTC : :::	2930 CTGTCAAGGTCC::::: CTGTCAT	3000 TGGCACATG	3070 TGTGATGTC
2850 .GCCTGGAATT ::: .GCAT	2920 29 AAATTTACCTGTCAA ::::::::	2990 GTAAAAATGA : G	3060 .GGGGCAGGAC : 'TG
0 2840 28 TCGGAATATAAGGAGCCTG : :::::::::::::::::::::::::::::::::::	2910 rccrccaaa	970 2980 TGCCTATCAAATCCGTG' :::::::::::::::::::::::::::::::::::	3050 ATGGTTTCAAGGG ::::. : TTCATTG-
2830 5TGAAGTCGG/ : :.	2890 2930 2940 2940 2930 2930 2940 ATAAACTTTTACTCACAACTCCTGTCCTGTGAGGTCCTGTGGAT :::::::::	2970 CCCCTGCCTA' :::. GCCTT' 1150	3030 3040 3050 3060 3070 3080 TACCGATGCACCTGTCCATATGGTTTCAAGGGGCAGGACTGTGATGTCCCAATTCA::: ::: ::: :::: :::::::::::::::::::
2820 TCCGACTGGC	2890 SATAAACTTT	2960 CTAAGTGTAA(:.	3030 ITACCGATGC: ::. AAGCCGT
2810 2850 2840 2850 2870 Slit ACATGCAGTGATTGGGGGAATATAAGGAGCCTGGAATTGCTCGTTGTGCTGGTCC :::: :::::::::::::::::::::::::::::::	2880 Slit TGGAGAAATGGCAGA : 325 T	2950 2960 3000 3010 GTCAATATTCTAGCTAAGTGTAACCCCTGCCTATCAAATCCGTGTAAAAATGATGGCACATGTAATAGTG : ::::::::::::::::::::::::::::::::::	3020 ATCCAGTTGACTTT .::: :: GTCCTTA
Slit ACAT :::: 325 ACAT 1090	Slit 325	Slit 325	Slit 325

Fig. 2M-11

3150 ATGGATTC :: :: TGCAAAC 1230	3220 AGATAATG : G	3290 3AGTATAC	3360 ATTCAAAG
3140 3150 AGGAGAAGAAGATGGATTC ::.::::::::-::-:-:	3210 NTGATTGTGAA	3280 TTGCCCACCTC	3350 rgccagcac <i>g</i> ?
3130 CTTAAAGGAAG ::: CTTG	3200 GTCAACGTTGA GENERAL :	3270 ACACATGCCTTTGC ::::::::::::::::::::::::::::::	30 3340 AGGACCTGAACCCCT ::: ::::GTCAGAATCCCC- 1290
3120 AACTTGCCACTT, ::. : ::: CTAATC-CTT 1210	3190 AATTGTGAAG	3260 TTAATAACTACAC: ::::: TCTTCA-	3330 TGCCCAGGAC(: ::: TTGTC/
3110 4ACATGGAGG	3180 IGAAGGAGAA	3250 GTCGATGGCATT ::::: TAGCAT- 1260	3320 GCTGGACTTCTGTG :::::: TCTAAACATCTATT 1280
3100 ACCCATGTA/ ::.:.	3170 TGATGGATT	3240 TCTACATGT	3310 3AGGAGAAGC' : :
3150 3140 3150 3150 3150 3140 3150 3140 3150 3140 3150 3140 3150 31it TGCCTGCATCAGTAACCATGTAAACGAACATGGAACTTGCCACTTAAAGGAAGG	3160 3170 3180 3190 3200 3210 3220 3220 3220 3210 3220 322	3230 3240 3250 3260 3270 3280 3290 Slit ACTGTGAAATAATTCTACATGTGTCGATGGCATTAATAACTACACATGCCTTTGCCCACCTGAGTATAC :::: ::::::::::::::::::::::::::::::::	330 3340 3350 3360 AGGTGAGTTGTGAGGAGCTTGTGCCCAGGACCTGAACCCCTGCCAGCACGATTCAAAG ::.:::::::::::::::::::::::::::::::
Slit 325	Slit 325	Slit 325	Slit 325

1290 **Fig. 2M-12**

DOVERELL DIEGEL

O (1)	O () d'	o v v	000
3430 ATCG	3500 CTATAC ::: ATAA 1360	3570 TACC . :	3640 ATGTC ::::
GAC.	35 GCTAT :: AT 1360	TCG . : AAG	ATA : : A-A
LIGC	ACG	CCCT. : :: CACA. 1410	30 3640 AGCCAATATGTC :::::: CAA-ATGGC 1450
3420 ACAC	3490 GTGA	3560 TCCT(:::	3630 .TGAG
IGAA	GCAC	3560 3 ATGGTCCTCCCTCGT::::::::::	3AA7
AGG.	GAT(CCAT(:: AT/ 1400	AAT?
3370 3380 3400 3410 3420 3430 TGCATCCTAACTCCAAAGGGATTCAAATGTGACTGCACACCAGGGTACGTAGGTGAACACTGCGACATCG ::::::CATCCATGCGTGGCAGAGCATTACGTT	3440 3450 3460 3470 3480 3490 3500 ATTTTGACGACTGCCAAGACAAGTGTAAAAACGGAGCCCACTGCACAGATGCAGTGAACGGCTATAC :::::::::::::::::::::::::::::::::	540 3550 3560 357 GAGTTTTCTCCACCCATGGTCCTCCCTCGTAC ::::::::::::::::::::::::::::::::::	3590 3600 3610 3620 3630 3640 TTTGATTGTCAGAATGGAGCTCAGTGTATCGTCAGAATAAATGAGCCAATATGTC :::::::::::::::::::::::::::::::::::
3 3GTA :: TTA	3 71GC : :	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	3 CGT:
CAGGG' T	34 3CCCACTGCA : .: :: CATCTTCA	540 SAGTTTTCTCCAC : : : : . : : : : : : : : : : :	3TAT :::: 3TAZ
3400 .ACAC(.:: .GCA	3470 GAGC(3540 TGAGTT : -GTAAA	3610 3620 AGCTCAGTGTATCGTCAG ::.::::::: -GCATAAAGTAACCA-
340 3TGACTGCACA ::::::::::::::::::::::::::::::::::	3 CGG	3.TGT	367 GCTCA(:::: GCATA)
SACT	4AAA 4	GTTC GTT-	3GAG:
3390 340 ATGTGACTGCACA ::::::::::::::::::::::::::::::::::	3450 3460 AAGACAACAAGTGTAA:::::::::::::::::::::::::::::	3530 CAGTGGCTTGTTC :. ::: ::: CTTGGGCT-GTT- 1380	3600 .GAATC : .G
3 AAA 	3 AGT .:: TGT	353 GTGGCT :::: TGGGCT 1380	90 360 GATTGTCAGAA ::: ::: GATGGCCTG 1430
TTC	AACA : . AAAT	CAG:	:TGT: :
3380 AGGGA	3450 AAGACAA : . ::: ATTACAA	3520 .GGTTA : .G	3590 TTGATT ::: GATG
33. AAA(34 CAA(:.	0 CCCCGAAGG ::.:: CCAGAG- 1370	3. TTTT:
TCC	L GCC	0 ccccGA :: ccAG	3580 AGCCCTGTGATAAT': : : ::: TACTGCGCTAAT
3370 ::::::	3440 ;ACGAC :: AC	3510 ATGCC	3580 TGTGATAA :: :::: TGCGCTAA
3370 CATCCTAAC :::::: CATCCATGC	34 1GAC :	35 ATAT ::	3580 3580 357 350 1420
3CA1 ::: -CA1	344 ATTTTGACG ::.::: ATATTAAC- 1330	GTGCAT.:::	GCC(.: AC
			t Ai 5 Ti
Slit 325	Slit 325	Slit 325	slit 325

Fig. 2M-1.

TOYBOAT OF TOP

3710 AAAGAGTC :. TGGGAA 1500	3780 CAGATGAA .:.: TTGGTAA-	3850 GGGCGTGTTC :::: GCAAATAC 1590	3920 SATGGAAA : :
3690 3700 37 GTGTGAATTTTATAAACAAAGAG :::::::::::-:::-::-:-:-:	3740 3750 3760 3770 3780 TTCGGCCTCAGACGACATAACACTTCAGATTGCCACAGATGAA :::.::::::::::::::::::::::::::::::::	3840 CTATCGGGG(::::	900 3910 GTGGAGACAATCAATGAT :::::::::::::::::::::::::::::::::
3690 AGTGTGAAT ::::: TGAGAAC	3760 TAACACTTCA :: TTTTTCAAGA	3830 GCGGTAGAACTCTAT :::::::::::::::::::::::::::::::::::	3900 AGTGTGGAG . :::: TTGGAA 0
3680 AAATTGGTT:::	3750 AGACGAACA::::::::::::::::::::::::::::::	3820 GACCATATCGC :: :: CAGC 1570	3880 3890 3 CCAGCTTCTGCCATTTACAGT : :: :::::
3660 3670 3680 3690 3700 3710 ATCAGGGAGAAAAGTGTGGTTAGTGTGAATTTTATAAACAAAGAGTC ::::::::::::::::::::::::::::::::::::	3730 3740 3750 3760 3770 3780 TTCAGCCAAGGTTCGGCCTCAGACGAACATAACACTTCAGATTGCCACAGATGAA ::::::::::::::::::::::::::::::::	3810 3820 3830 38 GGTGACAAAGACCATATCGCGGTAGAACTCTATC ::::::::::::::::::::::::::::::::::::	3870 3880 3890 3900 3910 3920 CCGGCTCTCATCCAGCTTCTGCCATTTACAGTGTGGAGACAATCAAT
3660 ATCAGGGAGAAAAG ::::::: GGAAAATAC 1470	3730 TTCAGCCAAG :.: TAC	3800 CTGTATAAGG : : : CATTA	3870 CCGGCTCTCA
3650 Slit AGTGTTTGCCTGGCT ::: :: :: 325 AGTCCTCT 1460	3720 373 TTATCTTCAGATTCCTTCA :.:::::	3790 3810 3820 3830 3840 3850 GACAGCGGAATCCTCTGTATAAGGGTGACAAAGACCATATCGCGGTAGAACTCTATCGGGGGCGTGTTC :::::::::::::::::::::::::	GACA
Slit AGTG: ::: 325 AGT 1460	Slit TTAT0	Slit GACA(3860 Slit GTGCCAGCTAT :.:: 325 AA-CTTACTA- 1600

Fig. 2M-14

ISPESSI CITION

3990 CCCAAA	4060 TGCCAG	4130 CATCCG	4200 CCTGGC
3980 ATGGTGGGAAC .::::: AGGGAA	4050 FGTAGGAGGCA'	4120 FTCCACGGCTG(::	4190 AAACAGGCATTTTG(::::: TTTTAATCATTTT
3970 rcttffccgrgg/ :.:::: -caargrc1660	4040 TCCACTCTA	4110 GGAACCAGCTT : :::: GCTAGCTT 1730	4180 CGATGCAAA(TTT
3960 AGTCTCTTTT :: CAAT	4030 ATTTTGACTC :.::: AAGTTGA	4100 TGGGCAGAACGG : .:: .: : TTGACATTTTG- 1720	4170 CAGAAGGTGC ::: GTG- 1750
3950 CTTGGATCAG	4020 4030 FCCACTCTGAATTTTGA::::::::::::::::::::::::	4090 3CCAGGCCCC	4160 SCAGGACTTC
3940 ACTACTTGCC ::::::	4010 TCAAAGCAG1 : T	4080 CATCTCTGCC :::	4150 .CAGTGAGCTG : :::
3930 3940 3950 3960 3970 3980 3990 Slit CTTCCACATTGTGGAACTACTTGGATCAGAGTCTCTTTGTCCGTGGATGGTGGGAACCCCAAA ::::: .::: .::::::::::::::::::::::::	4000 4010 4020 4030 4040 4050 4060 it ATCATCACTACTTGTCAAAGCAGTCCACTCTGAATTTTGACTCTCCACTCTATGTAGGAGGCATGCCAG ::::::::::::::::::::::::::::::::::	4070 4080 4090 4100 4110 4120 4130 Slit GGAAGAGTAACGTGGCATCTCTGCGCCAGGCCCCTGGGCAACGGAACCAGCTTCCACGGCTGCATCCG :::::::::::::::::::::::::::::::::::	4140 4150 4160 4170 4180 4190 4200 Slit GAACCTTTACATCAACAGTGAGCTGCAGGACTTCCAGAAGGTGCCGATGCAAACAGGCATTTTGCCTGGC ::::::::::::::::::::::::::::
S1i	Slit 325 167	32,	Slit 325

Fig. 2M-15

DOTESTI DITUTI

Fig. 2M-16

DOVERNAL DITORA

4540 4550 GGACAGCTGTGATCG ::: :: :::: -GACTTCA-TAAACA 1940	4620 TTGCCAA ::: :	4690 ACCGCTGA : :	4760 3AGAAAGT ::: ?AAA
4540 3GGGACAGCT ::::::	4600 4610 AGCAGCAGGGCTATGCTGCTTG ::::::::::::::::::::::::::::::	4680 4 GTGCTGTGGACCGC ::::::::::	4750 TGGACGAGGTTGAGA :::::::::::::::: TGGACATGATTTAAA 2050
4500 4510 4520 4530 4540 4550 TGGGGCAGCCCTACTGTGAATGCAGCAGTGGATACACGGGGGACAGCTGTGATCG :::::: -GGAGCAGGACTTCA-TAAACA 1930	4570 4580 4590 4600 4610 4620 AGGGGAAAGGATAAGATTACCAAAAGCAGCAGGGCTATGCTGCTTGCCAA ::::::::::::::::::::::::::::::::::	4640 4650 4660 4670 4680 4690 TCCCGATTAGAGTGCAGGGTGTGCAGGAGGGCAGTGCTGTGGACCGCTGA :::::::::::::::::::::::::::::::::::	4740 CTTTG
4520 ATGCAGCAGT	4590 TATTACCAAA	4660 GTGGGTGTGC	4730 TGACGGCTCCTC .:.: ::. TCAGTGCCA-
4510 CCTACTGTGA	4580 AAGGATAAGAGAT .:.:.:: -TGAAAATGAG	4650 3AGTGCAGAG	4710 4720 AATACTCTTTCGAATGCAC ::::::::::::::::::::::::::::::::::
		4640 STCCCGATTA(4710 AAATACTCTTT ::::::: ATATTGTCTAT 2020
4490 Slit GCAGGCTTTCAGGTC :::::: 325 CCTGGCTT	4560 Slit AGAAATCTCTTGTCG :: :: :: :: : 325 AATTGT-TCC	4630 Slit ACAACCAAGAAGGTG ::::: 325 ACATTC	4700 Slit GGAGCAAGCGGCGA ::::: 325AACTAAA
ഗ	S	S	Ω

Fig. 2M-17

OOZEESII OIIJOSI

4820 4830 TCTTTGGAAAAGGTTG ::: ::::: -CTTATATAATTA	4900 TAAAATAC :::: TTAA	
4820 IGTCTTTGGAA ::: :: CTTAT 2070	4890 AAATATATTG ::::::: AAATATGTTT 2130	
4810 CCGCCAGCTC	4870 4880 4890 TTCATAGTGGAAATATTTGAAATATATTG :::::::::::::::::::::::::::::::::	4950 rgcarrrg ::
4800 CTAAACACACTCC ::: :: AAACCTC- 2060	4870 TTCATAGTGC::.	4940 ACTTTTTTCTGCA .: : :: 5CGGCCGC-
4790 GTGTGTCCTAA :: AA	4860 TAATGAATGC::::::: TAATGAATTA	910 4920 4930 ACTTATTTATTATGAGAATAAAGACTT' :::.::::::::::::::::::::::::::::
4780 CTGTACGAGGT ::: CTG	4850 CATGTGGGAC' :: TGGAATA' 2090	4920 TTTTATTATGE:
4770 4780 4800 4810 4820 4830 Slit GGTGAAGTGCGGCTGTACGAGGTGTGTGTCTTTGGAAAGGTTG ::: :: :: :: :: :: :: :: :: :: :: :: ::	4840 ACTTCTTGAC :::: ::: ACTT-TAGT-	4910 4920 4930 4940 4950 Slit AGAACAGACTTATTTTTTTATGAGAATAAAGACTTTTTTTGCATTTG :::.:::::::::::::::::::::::::::
Slit G(325	Slit TAT7 ::: 325 TAT7 2080	Slit A 325 -

79 158 20 40 9 80 234 294 354 414 474 100 534 GCAGCTCTGGGGGAGCTCGGAGCTCCCGATCACGGCTTCTTGGGGGTAGCTACGGCTGGGGTGTGTAGAACGGGGCCGGG GCTGGGGCTGGGTCCCCTAGTGGAGACCCAAGTGCGAGAGGAAGAACTCTGCAGCTTCCTGCCTTCTGGGTCAGTTCC CTA GAG CAG GTA GCG GCG ď Ц > 团 ď Ø TTATTCAAGTCTGCAGCCGCTCCCAGGGAGATCTCGGTGGAACTTCAGAAACGCTGGGCAGTCTGCCTTTCAACC CIG GTG CAG GGC GAG CTA 니 > Ы Ø Q 口 CTG GAC GTG GIG TCC GAA Д > ഗ > 闰 CTG GAC CAG CGC GCA TCA Ω Ø ഷ ď വ ACC GCC GGC AAC CIG GGG 니 ŋ ⊱ ტ ď Z CGC TGG GAG GGC CGA GAG 闰 വ U 闰 വ 3 GCC TAC CTG TAC GAA CTG ᆸ ≻₁ ᆸ ď × 团 GAG TIC GGC GCT CIC GAG H 回 Ö ď 山 [I] GTG CCT GCG CCG GGT IGC U ტ Ø വ > വ GAC GGG GCG AGC TCAഗ r Ø Д Ω Ŋ GGC GTG TGG PCCC CTG GTG 口 \triangleright > U Z GAC ATG IGC AAA CGG CAT ر ا Ω × ĸ 耳 Σ GCA CTG GAG CGG GCT CTT Ц Ы ഷ ø ø 团 GCC GAC CCC GGC GGG TGG Д ᠐ Д ט Þ ⋈ TAC AAC GGA ACA CAG GCA Ø ტ ď × z ⊟ CIG GIG CGC GGC AAA TTT 口 Ö > × R ᅜ TCC TCC CTG CAA CCA TCA 口 Q വ Д ഗ ß CAC CCC CTG GGG GCA GTG ט Д CCC L GTG CCG GTG CTG > > Ц ATG CCG CTG T ACT CAA CTA Ы Ы Ø

ig. 3A

654 220 894 160 180 200 834 954 774 1014 280 S AGC R E R Y TAC P CCA LCTC H CTA P S TCC Q CAG I ATC W TGG S TCA П A GCA A GCC GGG H CAC CAC L CTG P ŋ 呂 P K AAG P AAT ACC N AAT P CCT Z ⊣ S AGC F TTC ATG GGT S AGC I ATC Q CAA P CCC Ü Σ g GGC GGC S S AGC AGG D GAC PCCT Q CAG വ് GAG N AAT R CGT CGC Q CAA E G GGG α 口 L D GAC P S AGC S AGC A GCT LCTT E GAA S TCA T ACA S TCC Q CAG CCT G GGC S AGT Д ACG P C TGC GTG LCTC R AGG Γ H \gt AGC ICC T ACA L TIG L GTG C TGC 口 \gt ഗ V GTC P GCC GGC CAC GGC K AAG s TCT ď Ŋ 耳 \mathcal{Q} R CGG PCCT A GCA K AAA TTC CCT GCC L CTC ш Þ Д V GTG L CTG V GTC M ATG E GAG CAT E GAG H L ACC GAG TCA A GCT ICC GCT Н 団 വ ß Ø GTG CTG ACG ACC GTG G GGA LCTT \triangleright ᆸ H ⊣ GAC GAA G GGC GTC GTG $_{
m TTC}$ 召 Ω \gt 团 \gt CAG TGG GCC TCC R AGA TGT Ø ⋈ Þ \mathcal{O} ഗ GGC T ACC G GGC R CGG GCT GTG ACT Ø > ⊱ E GAG H I ATT L V GTG LCTG S TCT

Fig. 3B

300 320 360 380 400 420 Γ TTG CAG AGG SCC CCC Д T ACT CIC GCC N AAT CGG AGA GAG S TCT П ĸ 口 D GAC GAC S AGC GCA AAG ATC CTG GAA Ø × Д 闰 G GGG V GTC GAA GCC CGC Γ CC GGG S AGT 闰 ഷ r ß D GAT I ATC Q CAG AAC H CAT CGG GTA ATG 엄 > Σ \mathbf{z} V GTG C TGC GTG GAG GIG $^{\mathrm{P}}$ CAT AGT 出 \triangleright വ V GTC D GAC GGT TAC GAG R CGA AGG ᠐ വ് ß 口 VGTA YTAC L CTT GTG CGA ACC GAG TGC > α ⊣ \mathbf{c} 口 GTG CTG GGG I ATC ICC CCG AGC V GTT > ഗ Ц ഗ Д GTG S AGT G GGC D GAT ATG ACC CAG AGT > Ø Н ഗ P CCC CIC CTG AAC S AGC AGC \triangleright > 口 വ Z GAC GTG AGG L CTG H T ACT TCG E GAG > ß Д α V GTC AAG E GAG A GCC GTG GAG CCC PCCT > × 闰 Д Q CAG GAG GAC CIC G GGG GTG T ACT > Ы Ŋ 闰 Ω TACC STCT GIG TAT ACG AGT വ \vdash GAT GAT AAA CAC О Ц Ω П \bowtie 出 AGG CTG CAG CAT P CCA P CCT α Ω Ø Ή JCC CAC P S TCA CTT 耳 Ц S \triangleright Η S TCC CAG C TGC CAT GGC F TTT Ø Σ 出 Ö CIGGAG F K AAG FTTC CAG G GGC Ы 臼 Ø

Fig. 3C

460	1614	480	1674	200	1734	511	1767
ᄓ	CIG	Q	CAG	ტ	GGC		
闰	GAA	×	AAA	Z	AAT		
H	ACT	Н	ATC	U	GGC		
Ø	CAG	U	GGC	⊱	ACG		
H	ACA	闰	GAA	Д	CCC		
闰	GAA	О	GAT	×	AAG		
Н	ATA	Ø	CAG	Ø	GCC		
闰	GAG	Д	GAT	ద	CGG		
씸	AGG	凶	GAA	Ц	CTA		
\triangleright	GTG	闰	GAG	⊱	ACC	*	\mathtt{TGA}
	ACG	臼	GAG	ŋ	999	>	GIC
⊱	ACC		GAG	Z	AAT	Н	CIG
Ц	CIG	Ø	CCC	団	GAG	H	CAC
⊱	ACG	ద	CGG	Ø	CAG	ტ	GGA
ഗ	ICC	ტ	999	>	GTT	ద	CGG
≯	TAC	ഗ	TCT	ഥ	TTT	ტ	GGG
യ			GGC	H	CAT	Z	AAT
ద	CGC	Д	CCA	Z	AAC		ATC
ტ	GGC	ഗ	TCT	Σ	ATG	X	TAC
田	GAG	Ц	CTG	Ø	CCC	Н	ATC

1846 1925 2004 2083 2320 2399 2478 2557 2162 2241 CCCAGGCCTGCCTCCCTTCCCTAGGCCTGGCTCCTTCTGTTGACATGGGAGATTTTAGCTCATCTTGGGGGCCTCCTTA CTGACTGTGTGTGTGTGGAGGGGTGACTGTCCGTGGAGGGGTGACTGTGTCCGTGGTGTGTTATTATGCTGTCATATTATCAG GTTACAGAAGCCCTCTGCCCTCTGGTGGCCTCTGGGCCTGCTGCATGTACATATTTTCTGTAAATATATACATGCGCCGGG CATGTGGCTGTGTGTGTCTCTGCCTGAAAAGCAGGTATTTTCTCAGACCCCAGAGCAGTATTAATGATGCAGAGGTT GGAGGAGAGAGAGACTGTGGCTCAGACCCAGGTGTGCGGGCATAGCTGGAGCTGGAATCTGCCTCCGGTGTGAGG PTTTATTTATTTTTTTTTTTTTTTTTTTTAGAGATGGAGTCTCACTATGTTGCTCAGGCTGGCCTTGAACTCCTGGGC SAACCTGTCTCCTACCACTTCGGAGCCATGGGGGCAAGTGTGAAGCAGCCAGTCCCTGGGTCAGCCAGAGGCTTGAACT

Fig. 31

3505 3189 3426 2873 2952 3031 3110 3268 3347 TCTGGCCTAAGGGAGAGGCTCCCATCCTTCGTTCCCCAGCCAAGCCTAGGACTTCGAATGTGGAGCCTGAAGATCTAAGA GGCACCTGAGAGCTGGTAGAGTCTGAAATTAGGGATGTGAGCCTCGTGGTTACTGAGTAAGGTAAAATTGCATCCACCA GCAGTGATTATAGACCGAGAGAGTAGGAGTTGAGGTGAGGTGAAGGAGGTGCTGGGGGGTGAGAATGTCGCCTTTCCCCC TGGGTTTTGGATCACTAATTCAAGGCTCTTCTGGATGTTTCTCTGGGTTGGGGCTGGAGTTCAATGAGGTTTATTTTA TCAAGCAATCCTCCTGCCTCAGCCTCCCTAGTAGCTGGGACTTTAAGTGTACACCACTGTGCCTGCTTTGAATCCTTTA CGAAGAGAAAAAAAAATTAAAGAAAGCCTTTAGATTTTATCCAATGTTTACTACTGGGATTGCTTAAAGTGAGGCCCCT GCTGGCCCACCCAGATACACTCAGCCAGAATACCTAGATTTAGTACCCAAACTCTTCTTAGTCTGAAATCTGCTGGATT

Fig. 3E

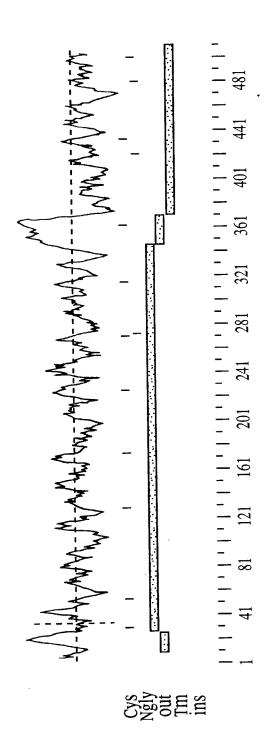


FIG. 3F

DOVERSIL OILUGUL

118 59 178 79 238 9 298 119 358 139 418 159 TACC S TCC A GCT A GCT GAT TCT CTA Д ᆸ ഗ GTG CTT GGA CTG CTG GAT GAC Ы υ Ц П Д Д ACC GIG TIC GAA CGG AGG GTG CCA > ப Д α ഷ ഥ GIC \mathtt{TGT} S TCC AGA ACA CCC TCA Q CAG ഷ Н ഗ gaa ACT GIG GGC TGG TTTTCC AAG ᠐ ¥ > Z ഗ ᄄ GCT CIG CAC I ATT AAC GGC GGG TTC긔 王 ᠐ ט ഥ z $_{
m LCI}$ ഗ CCA CIC CAC TAC TIG GAG TCT工 Ц 口 ß Д \succ CGC CAG I ATC TGG TCA ACT AAT GAC Q ഗ О Z Ļ z IGG വ GGG CAC CCC GAC S AGC Γ GAA ᠐ Д H Щ 闰 CAC AAT GIC ACC AAT CCIGGG Q CAG Д Ü Þ z ⊢ z AAG × ATG I ATC CAT P CCC CAA CCC GAT Ω Q Д 口 Σ TTCAGC AGG GAC Q CAG GTG TGC GAC > U Д വ ద Ω $_{\rm LCC}$ Ø CGC CAA GAA GGG CGA GIC GCA Ø ĸ O 闰 ᠐ വ് > CGT ፈ AGC TAC GAC CTT CTT GAA GTA Ω Ц ഗ Ы ப > × AGC ഗ CCI CAG ATC GTT GGC AGT GGG Ø > Д Ŋ ტ Н Ø ICC Ŋ GTG GGC GAT CIC AGG CTG AGT Ω > П ഷ Ц Ŋ ტ ACG AGC GTG TIG CCC CIG GTG TGC U Ŋ > ᆸ > Д ACA CAC GGC AAG CTG ACT ᠐ × H വ GGCGTC gccCIC GAG CCT CCT Ы ഠ GGG T ACT Q CAG E GAG M ATG CAT 工 U ט

Fig. 3G

G GGG

N AAT

E

Q CAG

V GTT

F TTT

H

N AAC

M ATG

A GCC

Q CAG

K AAA

I ATC

g GGC

E GAA

D GAT

Q CAG

D GAT

E GAA

E

					•				
179	538	199	9	219	658	239	718	259	7
>	GTG	×	AAA	H	CAC	⊢	ACG	闰	GAG
Ц	CTG	Ø	CAG	Ħ	CAT	⊢	ACC	ы	GAG
ᆸ	CTT	₽	ACC	ഗ	ICC	Ц	CTG	Ą	CCC
ט	TGC	Σ	ATG	H	CAT	⊢	ACG	ద	CGG
ഥ	TTC	Ø	CAG	Ц	CTG	വ	ICC	ט	GGG
П	TIG	Ø	CAG	ద	AGG	¥	TAC	ഗ	$_{ m LCL}$
П	CIC	Ø	CC	ద	CGG	യ	AGT	Ö	CGC
Ø	GCA	X	AAG	Н	ATC	ഷ	CGC	Д	CCA
A	BCC	ద	CGC	ß	TCC	ტ	GGC	ഗ	$_{ m LCI}$
н	ATC	껖	CGG	Z	AAC	臼	GAG	Ц	CTG
>	GTG	н	CAT	臼	GAG	Д	מממ	П	CIG
ტ	GGT	≯	TAC	ద	AGG	田	GAG		GAA
>	GTG	ద	CGA	⊢	ACC	闰	GAA	H	ACT
>	GTG	വ	ICC	Ы	CTG	ഗ	AGT	Ø	CAG
Λ	GTG	Σ	ATG	⊢	ACC	Ø	CAG	⊢	ACA
Λ	GTG	ᄓ	CIC	ᄓ	CIG	ഗ	AGC	臼	GAA
യ	ICG	>	GTG	臼	GAG	ద	AGG	Н	ATA
Ø	CCC	>	GTG	臼	GAG	д	CCC	臼	GAG
വ	TCA	>	GTG	臼	GAG	Ω	GAC	ద	AGG
>	GTG	>	GTG	X	TAT	H	ACG	>	GTG

299 898 300 VGTC L CTG H GGA R CGG G G G N AAT I ATC Y TAC I ATC g GGC N AAT g GGC T ACG P K AAG A GCC R CGG L CTA TACC

* TGA

NGTEELT OITGOT

CCCAGGCCTGCCTCCCTTCCCTAGGCCTCCTTCTGTTGACATGGGAGATTTTAGCTCATCTTGGGGGCCTCCTTA	980
AACACCCCCATTICITGCGGAAGATGCTCCCCATCCCACTGACTGCTTGACCTTTACCTCCAACCCTTCTGTTCATCGG	1059
GAGGGCTCCACCAATTGAGTCTCTCCCACCATGCATGCAGGTCACTGTGTGTG	1138
CTGACTGTGTGTGTGTGGGGGGGGGGGTGTCCGTGGAGGGGGTGACTGTGTCCGTGGTGTGTGT	1217
AGTCAAGTGAACTGTGGTGTATGTGCCACGGGATTTGAGTGGTTGCGTGGGCAACACTGTCAGGGTTTGGCGTGTGTGT	1296
CATGTGGCTGTGTGTGTCTCTGCCTGAAAAAGCAGGTATTTTCTCAGACCCCAGAGCAGTATTAATGATGCAGAGGTT	1375
GGAGGAGAGAGAGACTGTGGCTCAGACCCAGGTGTGCGGGCATAGCTGGAGCTGGAATCTGCCTCCGGTGTGAGG	1454
GAACCTGTCTCCTACCACTTCGGAGCCATGGGGGCAAGTGTGAAGCAGCCAGTCCCTGGGTCAGCCAGAGCTTGAACT	1533
GTTACAGAAGCCCTCTGCCCTCTGGTGGCCTCTGGGCCTGCTGCATGTACATATTTTCTGTAAATATACATGCGCCGGG	1612
AGCTTCTTGCAGGAATACTGCTCCGAATCACTTTTTTTTT	1691
TTTTATTTATTTTTTTTTTTTTTTTTTAGAGATGGAGTCTCACTATGTTGCTCAGGCTGGCCTTGAACTCCTGGGC	1770
TCAAGCAATCCTCCTGCCTCAGCCTCCCTAGTAGCTGGGACTTTAAGTGTACACCACTGTGCCTGCTTTGAATCCTTTA	1849
CGAAGAGAAAAAAAAATTAAAGAAAGCCTTTAGATTTTATCCAATGTTTACTACTGGGATTGCTTAAAGTGAGGCCCCT	1928
CCAACACCAGGGGGTTAATTCCTGTGATTGTGAAAGGGGCTACTTCCAAGGCATCTTCATGCAGGCAG	2007
GGCACCTGAGAGCTGGTAGAGTCTGAAATTAGGGATGTGAGCCTGGTGACAAGGGGCTCCTGTTCAATAGTGGTGTTGGG	2086
GAGAGAGAGAGCAGTGATTATAGACCGAGAGTAGGAGTTGAGGTGAGGTGAAGGAGGTGCTGGGGGTGAGAATGTCG	2165
CCTTTCCCCCTGGGTTTTGGATCACTAATTCAAGGCTCTTCTGGATGTTTCTCTGGGTTGGGGCTGGAGTTCAATGAGG	2244
TTTATTTTTAGCTGGCCCACCCAGATACACTCAGCCAGAATACCTAGATTTAGTACCCCAAACTCTTAGTCTTGAAAT	2323
CTGCTGGATITCTGGCCTAAGGGAGAGGCTCCCATCCTTCGTTCCCCAGCCAG	2402
AGATCTAAGATCCTAACATGTACATTTTATGTAAATATGTGCATATTTGTACATAAAATGATATTCTGTTTTTAAATAA	2481
ACAGACAAAACTTGAAAAAAAAAAAAAAAAAAAAAAAAA	2510

Fig. 31

ngysesil nigga

! ! !	VAWARV 70	 GSFQAR 140	20		210	90 90PPPSY ::::::: 90PPPSY 280
	RGDSGEQVGÇ 60		10 20	NGIISSKSFANSASAVISETII :::::::::::::::::::::::::::::::::::	200	80 GAMLKCLSEC :::::::: GAMLKCLSEC 270
	ILLLLLLASFTGRCPAGELETSDVVTVVLGQDAKLPCFYRGDSGEQVGQVAWARV 20 30 40 50 60 70		QUUEEUA		190	60 70 80 9 ILHVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQP ::::::::::::::::::::::::::::::::::::
 	LETSDVVTVV 40	 PRNPLDGSVI 110		EGSPAPSVTW	180	60 FLAEASVRGI ::::::::::: FLAEASVRGI 250
 	SFTGRCPAGE 30	 YEGRVEQPPP 100			170	50 QRITHILHVS ::::::::: QRITHILHVS 240
	AWLLLLLLLA 20	 SKYGLHVSPA			160	40 50 VVSHPGLLQDQRITH: :::::::::::::::::::::::::::::::::::
	T364 MPLSLGAEMWGPEAWI 10		}	HILLAS CTARS CRANKS TO THE TABLE TO THE TOTAL TO SERVING TO THE TRANSPORT OF THE TRANSPORT	150	30 40 50 90 ALT VPSRSMNGQPLTCVVSHPGLLQDQRITHILHVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPPPSY ::::::::::::::::::::::::::::::::::
ALT -	T364 N	ALT . T364 I		ALT .	# 0 1	ALT '

Fig. 3.1

	100		110	120	130	140	150	160
ALT T364	NWTRLDGPLPSGVRV :::::::::::: NWTRLDGPLPSGVRV	PLPSGVR:::::	VVDGDTLGFPI::::::::::::::::::::::::::::::::::::	PLTTEHSGIY	VCHVSNEFS :::::::	SRDSQVTVDVI ::::::::: SRDSQVTVDVI	ALT NWTRLDGPLPSGVRVDGDTLGFPPLTTEHSGIYVCHVSNEFSSRDSQVTVDVLADPQEDSGKQVDLVSAS :::::::::::::::::::::::::::::::::::	LVSAS ::::: LVSAS
		290	300	310	320	330	340	
ALT	170 VVVVGVI	AALLFCL	180 LVVVVVLMSF	190 YYHRRKAQQM	200 TQKYEEELT	210 LTRENSIRRLI	170 180 190 200 210 220 ALT VVVVGVIAALLFCLLVVVVVLMSRYHRRKAQQMTQKYEEELTLTRENSIRRLHSHHTDPRSQ	1 1 1 1
T364		AALLFCL	SESSESSESSESSESSESSESSESSESSESSESSESSES	::::::: RYHRRKAQQM	:::::: TQKYEEELT	::::::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	SVGLR
ω.	350	360	370	380	390	400	410	
			230	240	250	260	270	
ALT		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SEEPEGI	RSYSTLTTVR	EIETQTELL	SPGSGRAEEE	SEEPEGRSYSTLTTVREIETQTELLSPGSGRAEEEEDQDEGIKQAMNHFVQEN	IFVQEN
					•••			••
T364	AEGHPDSI	LKDNSSC	SVMSEEPEGF	RSYSTLTTVR	EIETQTELL	SPGSGRAEEEI	T364 AEGHPDSLKDNSSCSVMSEEPEGRSYSTLTTVREIETQTELLSPGSGRAEEEEDQDEGIKQAMNHFVQEN	IFVQEN
4,	420	430	440	450	460	7.0	480	
	280	290						
ALT	ALT GTLRAKPTGNGIYINGRGHLV	IGNGIYI	NGRGHLV					
		••						
T364	T364 GTLRAKPTGNGIYINGRGHLV	TGNGIYI	NGRGHLV					
4	490	500	510					

Fig. 3K

DATES A LOT INDI

55 15 198 35 258 55 438 115 498 CTTAATGTTGGAAGTCTCTTAGTCCTATGAGAGTGTGTAGCAGTTTGTCCCTGAG CTCTAGCTTCTTTAAATGAAGCTGAGTCTCTGGGCAACATCTTTAGGGAGAGAGGGTACAAAAGGTTCCTGGACCTTCTC TGG TIC GCC TCT AGT GTT ø ſτι ß Z വ \gt GGC TGC CTG ICC CCA TIG Ö C Ц Д വ Ы AGA GCT AGG GTG ATT CAT ഷ ď 卍 > Н 口 AAA AGT AAA AAG TIC GCA ď ഗ ¥ ¥ ¥ ഥ GAG GGC CIC ACA TAC GGA 闰 Ы Ü Ċ [-× ACA CIC GGG IGC ACT ATG Н Н ₽ r U Σ AGT GCA GAA GAA AGT GAG Ø 团 ഗ 闰 വ 闰 CAA TCC ATT GGT AGT GTT O Н U വ ß > CCTTCC TIC TAT GGT IGI Ø Ö U Д × ഥ CAA ATT IGC AAC ACA TTTÖ O \vdash ഥ Z ⊣ CAG ACC CAG GGG TTTTCA U Ø ᇿ ⊣ ഗ O GAG CIC AAG GCT CAT GAG ď 耳 ᆸ × 团 臼 GTG TAC AGT CAA AGT TGG × ß Ø > വ Z ATG TCT ACT TCA TCT AAG E٦ × Σ ഗ വ ß ATG CAT TGG GTA GCT TCT \triangleright 耳 Ø ഗ Σ ⋈ AACACAGGGAGCCTGCATA CIC GTA TAT CCA TGG Д 口 > × ⋈ AGA TGT TCA TGC GTT Ö Ö > α ഗ CTG AGC CAC TGT AAG П 田 വ U × TCC GTG GAG CTA GGA വ Ц Ö 凶 TTG ATT TGG GAA GAA ы 闰 口 ≥ Н

Fig. 4A

TCT

TTT

TCA

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L	ACA	Ø	CAA	ш	GAA		
×	AAG	臼	GAG	ט	$_{ m TGT}$		
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Н		ഗ		>			
×	TGG	H	_	Ω			
Q	•	Z	. 7	Z	•		TGA
Z	•	വ	CCC	M	TGG	ᆸ	_
Z	AAT	团	GAG	ט	CGC	X	TAC
Z	•	U	GGT	M	TGG	Н	ATT
Z	AAT	ᆸ	CTA	U	GGA		AAG
ט	GGT	田	CAC	H	ACA	z	AAT
	CAA	M	-	Д	CCT		ATG
Д	CCA	Ĺτι	TTT	X	AAA	闰	GAG
О	GAC	ద	AGA	×	TGG	Ŋ	TGT
വ	TCA	\triangleright	GIC	ш	TIC	Н	ATA
П	CIT	z	AAT	>	GTC	W	TCA
ტ	GGG	×	AAA	Н	ATA	Z	AAT
ᄓ	CIG	ш	GAG	ഗ	TCA	ద	AGG
Ĺτι	$_{ m LLL}$	X	TAT	Ø	GCT	ద	AGA
X	TAT	Д	CCI	บ	IGI	H	ACT

862 1099 1020 1336 1415 941 1257 1494 1573 CTTTAATCAATCTTCTCGTTTCCTCTTTTCCATTAATGATAGAATGCACCCTTCCTCTTTGTTCCATTCTTTCACTT GTTATTCATTTTTTTTTCTTCACACTTCATTACACAAATATTTATTGTTTCAGAGACTGTACTATTTTGTTTAG GGCAACTTGGTGTTTGGCTATTTAATGTAACCTGGAAATTATTTTATTTTGCAGTTTGGGATTTTGGCATTTTATATGT ATCCATCATTITAAATGGCAATGATAATGACAGTTTATTTTTTATATATAAAAACCTCAACAAATTTTCCAAACAAT IACCAAAATGGTCATTAATCTGTATCCACAAGGATTTCTGCATTACATACTTTAAAACAAATTACCTAATTATTTAGT AAGCATTTCTTGTTACCCAAATCTAACCTATTCCTGAAATATGATGGTTAGCAAAGTTTGAGATAACTAGAGCCTGTA GTAGAAGCTTAATTGGAAAGAAGAAGAATTACTGACGTAATTTTTTTCCCTGACGTCTTTAAAATTGAACCCTATCAT GAAATGATAATTTCTTCCTGAATTTACACATAATCCTTATGTTATAGAGGTTCACAGAAATGGAAAGATACCTGTTTCC

ngyssin indi

3114	TAATAAAACATAGCAAAGCCTTTTAAAAAAAAAAAAAAA
3074	ACAAAGATTTCACACATGAATACCTATGTAACAAATCTCCATGTTCTACACATATACCCCCAGAACTTAAAGTATAAA
2995	AACTTTGCCCTAAAAGTTAAGACATATTCTGAGAATCATAATAGTCACATGATTTCTGATGCTATCTGCTCTGTTAATA
2916	TTAAATTATTGAAGTCTGAGTTTTCAAAAGTGATTTTTTCCCACAAAGGTGCCAACACTTAAGCTAGAGGTTGTT
2837	ATGAATCATTAAGACAGTAATTAGGAGTTCACAAATTTAAAACATTTCACGTAATTTTAAATTATTGTCTTCAATAATT
2758	AAAACTCCATGGTTTACAGGCATGTCATATTGAAAATAAAGCTGCAATAGCTTTTTTATACAATTATGCTCTCTCAAGAAA
2679	ACAAAATGTGTAACAAGAAACTAATGACCTTTCTAAAATCAAACATTCAATTATCTACAATGTCTATTTACAAACAGGG
2600	ACAACTTTTATTAGAAAAGTTATACATAACACAGCATCAACTATTTTCAAGAACCCAATAAGCAACAAAAAACCAGACTA
2521	TATATGGTTCTAAATCTATCTTACTAGGTGGTTTTCCATTTCCTCTGCTCCAAAATATTTTTTTT
2442	AAATTTTAAAAAATCCCAATATGGCAATCACCTTTTAGGTTAAAAATTTTAATCCATTTACATTTGTGACAATTCGACATA
2363	TGCTGTAAAATTTTTTTTCCATCTTCTATTTTTGACCATTTTTATTCCACATGTGCTCTTAATAAGTAGCATATAGTT
2284	TTCTTTAAATTTTAGTAATGCCTTTTGGCTTTTAATTTTTCTCCTGATATTAAAATAGATACAGTAACTTTCATTATGTTAG
2205	AGCCATGATGAGGTATATACAATGTTATAATTATTACTTGTACATGGCAAATTAATT
2126	GGCACAACAATTTTTAAATTTAATTTTAGCAAATATTTGGATATTAAAGCTTCTTATAGAAAGAGATACCTGTATATTTA
2047	ACTCATGAGCAACTTGAATAGTTGTAACTGTGATGCATATGTAGATTCTAACACATTTTTCCCCCTTGAATAGAAATTT
1968	TGGCAGTAGGAGCCTATAAAGGGATAAGCAATTGGGAAAGGATTGGGAAGTTGGTAGTACTGAACATCTTCTCACCTGG
1889	TTGCACTGAAAATACCATAATATAAAGAAGAATCCCATCATCCAAATTGAGCCTATATTGATTG
1810	GCATATTAAACTTATTGGTGGGCATGACTATATGCAACAGTTGCATGATATGATACAAATTATGTTATTTTTTTT

Fig. 4(

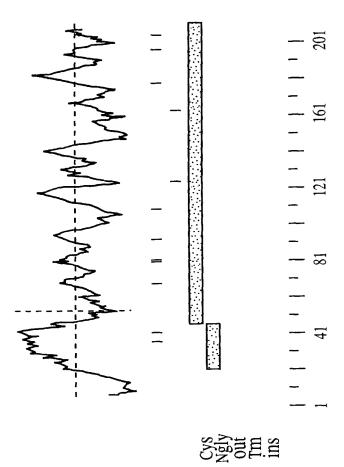


FIG. 4D

158 GAACTCCCCGGTGTCGACCCCGCGTCCCGATTGGCCCCGCTCTGTGGCCATTTAACTCAAGTGTGTGGAAGTTGATTCT SAACTCTGGCCTCTTTGACAGAAGCCAGGTCCCTGAGTCGTATTTTGGAGACAGATGCAAGAAACCCCTGACCTTCTGA

16 36 56 96 221 281 341 116 401 461 521 Γ S AGC CAC TGG AAG GIG TAC > 工 × ⋈ T ACC A GCG CTTATG T ACC GIG $_{
m TCT}$ > Н Ŋ Σ TGG I ATT GAA AAA CTGTCT ഗ Ц × JGC F TTC TAT GAA ATT CAT TCA Н 二 \succ ഥ GIC TGT CTA CIC GAG TCA GCT 口 U ø 口 ഗ GGA TAC ACC AGA GTG GGG AAT ŋ × H 吆 G Z \gt AAG AGA CTGAGT ATG IGC ATG ပ × Н ഗ വ Σ Σ GGG $\frac{1}{1}$ AGC CAG CAG AGT ACT Ŋ ഗ Ø O ഗ Н CAA CIC GGG TCC CCC GTT CAG O Ø Н S > U Щ ICC $_{ ext{TTA}}^{ ext{L}}$ CAG GGC GAA TGT ACC Ö Ŋ ഗ O ⊱⊣ ഥ ATC CAA M ATG GAC AAC AGT TTTO Ω ഗ ſщ Z Н AGA ATG ICC TIC CAG TIC TCA Ø œ ഗ S Σ GAA I ATT GAG AAT ATT AAG C TGC × Ы 口 Z Н CAG GIG TTT ACC $^{
m TGG}$ CAG AGT Ø O \triangleright 3 ഗ Ŀ CAC ACC GCT L CTC GAG CAA Ø 工 [L] O GCG GCT TAC AGC AGT AAT Ø Ø Σ ഗ z വ ACATACACCTCAACA S TCA ACT CCA IGG GAA S TCC Д ഥ Z ⊣ TGG GIG IGC TIC ACT CAT Ö 耳 L CTC STG $^{
m Y}$ IGC AAC AAT ပ \gt z AGA ACA GGA GAG $_{
m IGT}$ G 口 Еч

Fig. 4E

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CI	⊢	ICG	GAT	೧೦೦	AAG	GTA	ATG	GCA	AAT	299 1	AAT	GGA	TCG	ATG	ATA	CTC	CII	641
2;	_	S V K M S G S	Ŋ	ഗ	Ŋ	⊢	Д	Σ	Z	വ	Н	ᄺ	Ø	×	Ø	ტ	S V	176
AI	Ō	TCA	GGT	ICI	CGC	ACC	$\mathcal{C}\mathcal{C}\mathcal{C}$	ATG	AAC	CCA	ATC	GGC ACC CCC ATG AAC CCA ATC TTC CAG AAG A	CAG	AAG	AGC	CCI	GTG	701
																		179
TTT CAA TAG																		710
CCI	Ĕ	GAAZ	TGGG	TTTACTGGAATCCTTCGAAATGGGGCTGGGAATGATGTTTTCTGTGATAGTAAACACACAATTCAATATGTGAAATGAANA	GGAA	TGAT	GTTT	TCTC	STGA1	ragr?	AAAC!	ACAA.	LTCA	ATATO	STGA	AATG?	AANA	789
GAA	Ē	AGATTACCTATAATGCCTGTTATAATA	THAT	THOTE	A T A A L													821

Fig. 4F

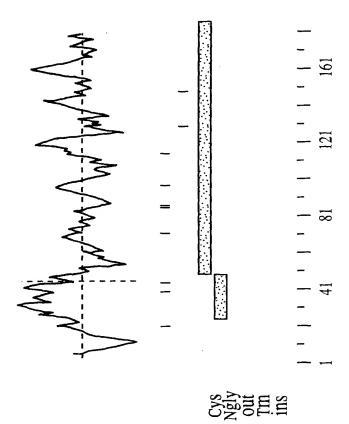


FIG. 46

IOPEKTI IIIOOT

0 : : : : : : : : : : : : : : : : : : :	닭 :: 닭	
LTCESI	ESFSY.	CEMNK. FQKSG
20 50 70 70 70 50 60 70 LSLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYHSSLTCFSEG .::::::::::::::::::::::::::::::::::::	90 100 110 120 130 KSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFSYFL :::::::::::::::::::::::::::::::::::	160 170 180 190 200 KTPYEKNVRFWHLGEPNHSAEQCASIVFWKPTGWGWNDVICETRRNSICEMNKIY : : : : : : : : : : : : : : : : : :
(LSELH ::::	EQNFI ::::: EQNFI	VICET :
50 3ETGKR :: DQPSRR 50	120 /FNTEP::::: /INTEP	190 3wGwnD : :
YHFTY(: . : . YQFIMI	GAHLVY ::::: GAHLVY	FWKPTGW : .: KMSGS 160
40 SCVVT:::: SCVVT:	110 incvemc :::::: incvemc 110	170 180 190 GEPNHSAEQCASIVFWKPTGWGWN : : : : : : : : : : : : : : : : : :
SACFIV	VSKSEÇ ::::: WSTSEÇ	70 PNHSAEÇ -GNGSMI 150
30 SIALLS: :. ::: SMLLLS	100 SEEKVW: . : : TKENFW:	170 HLGEPNI GI
WSVAGI:::::WSAAVI:	SCYFIS SCYLIS SCYLIS 90	NVRFW
20 .SLRLW .::::	SSFGSS	160 (TPYEKN)
EKRGWI : :GVC-W-	80 CPASWF::::	M I
10 QPQSTE : . : . QSQGKC	80 WGCCPA ::::: KMWGCCPN	1. QGNNNN : KVMAN.
1 MMQEQQPQS :.::.:. MVQERQSQG	TKVPA: :.: TMVSEKM 70	140 1 GLSDPQ ::::: 6 GLSDPK 140
10 human MMQEQQPQSTEKRGW :::::::: murine MVQERQSQGKGVC-W	80 100 110 120 130 human TKVPAWGCCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFSYFL ::::::::::::::::::::::::::::::::::::	140 150 human GLSDPQGNNNWQWID ::::: .: murine GLSDPKVMAN
		E

human L

murine Q

Tig. 4H

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0 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 & · fi	0 U ·· U	F+ ()
7 GTG GCT	140 CATA TTAT	210 AGGG ::::	TAC. TAC
TCT:::TCA:	TTA(::: TTA' 130	TGA:::	270 TCCAGTTGC' ::::::: TCCAGCTGC'
. : : : : :) : • : :AAT	CAG	:: :: AGC
60 ACTC ::::	130 FACC:::	200 3CTT	FTCC
GAG2 :::: GAG2 50	ACT: ACT: 120	CCTC::::::::::::::::::::::::::::::::::	260 1667 ::: 1667 260
20	4 · 9 	ICA ::: ICA	230 240 250 260 270 CTGGGGATGTTGCCCAGCTTCTTGGAAGTCATTTGGTTCCAGTTGCTACT ::::::::::::::::::::::::::::::::::
50 1GTC :::	120 IGTA(190 AGTC:	AGTC
3GT1 : : 3CTC 40	CTG1:::	TCA/:::::TCC//180	250 GGAF :::: GGAZ
GCT(:: TCT(GAG(::: GAG(CAT.	CTT(
40 GAG :::	110 1610 ::	180 TAT(::	CTT:
AAAA AAGG	TCAT:::'TCAT	CTCA:::CACA:	240 ITGCCCAGCTT ::::::: CTGCCCAAATC 240
3A <i>G</i> ? : • : : 3GG	3CTJ 3TTJ	ACAC	
30 ACA(:	100 CTT(CCT(170 ACT	
AGT	.:: .:: .GTA	150 160 170 180 AAACTGGCAAAAGGCTGTCTGAACTACACTCATATCATTCA : . : . : . : : : : : : : : : : : : : :	230 GGGGATG :::::: GGGGATG 230
CAA :: CA-	TCA::::TGA	GTC:	2 -166 ::::
20 ACC1 : :	90 CTCC :::	160 GGCT:::GACT	
GCAAC	GCA(: TTA(80	AAA(.::GAA(C AAAJ 20
GCA.		GCA:	
10 10 10	80 11100 11100	150 ACTG : .	220 7GCC ::::
IGCA IGCA	GAT7 :::: GAT7	TGAAZ :: :CCAGC	AAGGT::::::::::::::::::::::::::::::::::
10 20 ATGATGCAAGAGCAGCAACCTCAA ::::::::::::::::::::::::::::::	80 CTGGGATTTCCATT ::::::::: CTGTGATTTCCATG	GGT :- GAC	220 ACAAAGGTGCCAGC ::.:::: ACTATGGTGTCAGA 210
		150 human TGGTGAAACTGGCA : : : : : : : : : : : : : : : : : : :	
human murine	human murine	nume ırin	human murine
Tu lu	J M	Ju lui	I m

Fig. 41

		290	300	310	320	330	340
human		GAAGAGGAAGGT	TTTGGTCTAAG	AGTGAGCAGAACTGTGTTGAGATGGGAGCACAT		SAT'GGGAGCAC	ATTTGGT.
murine	TCATTICTACCAAGGAGAACTTCTGGAGCACCAGTGAGCAGAACTGTGTTCAGATGGGGGGCTCATCTGGT 280 330 340	AAGGAGAACTT 290	CTGGAGCACC. 300	AGTGAGCAGAA 310	SZO	sargegegere 330	ATCTGGT 340
human	350 360 370 380 390 400 410 TGTGTTCATTCATTTTCATTTTTTTTTTTTTTTTTTTTT	360 CAGAAGCAGAG	370 CAGAATTTCA	380 TTGTCCAGCAG	390 GTGAATGAG	400 rcattttctta	410 TTTTCTG
murine	::::::::::::::::::::::::::::::::::::::	:.:::::: CTGAAGCGGAG 360	::::::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	::: ::::: FCACTITCTIA 400	:: :: CTTCCTG 410
human	420 430 440 450 460 470 480 GGGCTTTCAGACCCCACAGAGATAATTGGCAATGGATTGATAAGACACCTTATGAGAAAAATGTCA	430 CCCACAAGGTA	440 ATAATAATTG	450 GCAATGGATTG	460 SATAAGACAC	470 CTTATGAGAAP	480 AATGTCA
murine	::::::::::::::::::::::::::::::::::::::	:: :::::: TCC-CAAGGTA 430	::::::::::::::::::::::::::::::::::::::	:::::::: GCAATGGATCC 450	::::: GATGATACTCC 460	::.:::::::::::::::::::::::::::::::::::	::::::: AAAATGTCA 480
human	490 540 550 520 530 540 550 6ATTTTGGCACCTAGGTGAGCCAATGTGCTTCAATAGTCTTCTGGAAACCTAC	500 CTAGGTGAGCC	510 CAATCATTCT	520 GCAGAGCAATG	530 TGCTTCAATA	540 AGTCTTCTGGA	550 AACCTAC
murine	::::::::::::::::::::::::::::::::::::::	: .:::: ccccargaacc 500	::::::::::::::::::::::::::::::::::::::	.:::::::::::::::::::::::::::::::::::::	:::::: GTTTCAA530		

Fig. 4.

DOPERLY DITORY

620	TAAGATTTAC
610	GTGAGATGAA
009	TGATGTTATCTGTGAAACTAGAAGGAATTCAATATGTGA
590	AAACTAGAAGGA
580	STTATCTGTGA
570	TGGAA
560	AGGATGGGGC
	human

murine --

human CTA

murine ---

ngyeestt briebit

50 60 70	TLRIWSAAVISMLLLSTCFIASCVVTYQFIMDQPSRRLYELHTYHSSLTCFSEGTM		ITLRLWSAAVISMLLLSTCFIASCVVTYQFIMDQPSRRLYELHTYHSSLTCFSEGTM	50 60 70	120 130 140	mT405 VSEKMWGCCPNHWKSFGSSCYLISTKENFWSTSEQNCVQMGAHLVVINTEAEQNFITQQLNESLSYFLGL		VSEKMWGCCPNHWKSFGSSCYLISTKENFWSTSEQNCVQMGAHLVVINTEAEQNFITQQLNESLSYFLGL	120 130 140	170	IFQKSGVFQ	:	Dectin SDPQGNGKWQWIDDTPFSQNVRFWHPHEPNLPEERCVSIVYWNPSKWGWNDVFCDSKHNSICEMKKIYL	190
40	IASCVVTYQFIMDQP		IASCVVTYQFIMDQP	40	110 1	EQNCVQMGAHLVVIN		EQNCVQMGAHLVVIN	110 1				ERCVSIVYWNPSKWG	180
30	VISMLLLSTCF.	•••	VISMLLLSTCF.	30	100	ISTKENFWSTS		ISTKENFWSTSI	100	0			FWHPHEPNLPEI	170
20	VCWTLRLWSAA	•••	VCWTLRLWSAA'	20	06	HWKSFGSSCYL		HWKSFGSSCYL	06	150 160	GNGSMILLSVK	•	IDDTPFSQNVR	160
10	mT405 MVQERQSQGKGVCW	•••	Dectin MVQERQSQGKGVCW	10	80	VSEKMWGCCPN	•••	VSEKMWGCCPN	80	-	mT405 SDPKVMANGNGSMILLSVKMSGSGTPMNP-		SDPQGNGKWQW	۲. د ت
	mT405		Dectin			mT405		Dectin			mT405		Dectin	

Fig. 4L

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70 FG: 70	01.10	XI.
C F S E	140 FSYFL .:::: LSYFL 140	ANKI ::::
SSLT(NES]	SICEN: .:
60 SYHS :::: TYHS	130 IVQQI ::::: ITQQI 130	200 TRRNS .::::
SELH ::: YELH	ONFI SONFI ONFI	ICET FCDS
GKRL :: SRRL	TEAE :::: TEAE	WNDV :::
50 YGETU	120 VVENT :::: VVINT	190 IGWGU :::: SKWGU
YHFT. : - : - YQFII	SAHLY SAHLY SAHLY	EWKP' .:. YWNP;
40 CVVT::: CVVT	110 NCVEM ::::: NCVQM(180 190 200 SAEQCASIVFWKPTGWGWNDVICETRRNSICEMNKI :.:.:::::::::::::::::::::::::::::::::
IVS(110 SEQNCV) ::::: SEQNCV(18 AEQCZ : SERCZ
SACI	WSK: :: :WST:	SNHS <i>i</i>
20	90 100 110 120 140 KSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESFSYFL :::::::::::::::::::::::::::::::::::	160 170 180 190 200 KTPYEKNVRFWHLGEPNHSAEQCASIVFWKPTGWGWNDVICETRRNSICEMNKIYL : .::::::::::::::::::::::::::::::::::
AGIS :::: AVIS	FISS	REWE :: Rewe
20 RLWSV ::::: RLWSA	90 GSSCY GSSCY GSSCY	160 KTPYEKNVRF :::::: DTPFSQNVRF 160
LSLR .:: -TLR	XX	160 KTPYE! :: DTPFS(
KRGW : VC-W		
10 28TE: :. 2GKG	80 WGCCPA :::::: WGCCPN	150 SLSDPQGNNNWQW :::::::::::::::::::::::::::::::::
1 MOEQOPOS MVQERQSQG	TKVPA :•:•: IMVSEKM	OPQGJ ::: OPQGJ
MMQI :::	TKVI :.: TMV	GLSI ::: GLSI
10 hT405 MMQEQQPQSTEKRGW :::::::: Dectin MVQERQSQGKGVC-W	80 hT405 TKVPAWGCCPASW :::::::::	150 hT405 GLSDPQGNNNWQWID :::::::::::: Dectin GLSDPQGNGKWQWID
h1 Dec	h1 Dec	h1 Dec

Fig. 4M

IDYKKKAA MITOOT

60 120 178	226	274	322	370	418
G GCATTTAACT C AGGTCCCTGA A CCTCAACA	TGG ACC CTG Trp Thr Leu 15	AGT ACC TGT Ser Thr Cys 30	GAC CAG CCC Asp Gln Pro	CTC ACC TGC Leu Thr Cys	TGC TGC CCA Cys Cys Pro 80
CCGCTCTGTG GACAGAAGCC TGAACATACA	TGC Cys	TTG	ATG Met 45	AGT Ser	GGA Gly
_	GGGA GTC S Gly Val	3 TTA CTC E Leu Leu	A TTT ATT n Phe Ile	CAT TCC r His Ser 60	A ATG TGG s Met Trp 75
G CAGCATTGGC C TGGCCTCTTT C CCTGACCTTC	GGG AAG Gly Lys 10	TCC ATG Ser Met 25	TAC CAA Tyr Gln	ACA TAC Thr Tyr	GAA AAA Glu Lys
TCTGGGTTTG TTCTGAACTC GCAAGAAACC	TCC CAA Ser Gln	GTG ATT Val Ile	GTG ACT Val Thr 40	CTT CAC Leu His 55	GTG TCA Val Ser
	AGA CAA Arg Gln 5	GCT GCT Ala Ala	TGT GTG Cys Val	TAT GAA Tyr Glu	ACT ATG Thr Met
TCCGCTGACT TGGAAGTTGA GGAGACAGAT	GAA Glu	TCA Ser 20	AGC Ser	CTA Leu	GGG
CGACCCCGCG CAAGTGTGTG GTCGTATTTT	GTG CAG Val Gln	CTC TGG Leu Trp	ATT GCG Ile Ala 35	AGA Arg 50	AGT Ser
CGA CAA GTC	ATG Met 1	AGA Arg	TTC Phe	AGT Ser	TTC Phe 65

DOYMANT NATIONA

466	514	562	610	658	706
AAG Lys	GCT Ala	CAG Gln	CAA Gln	AAT Asn 160	TGT Cys
ACC Thr 95	GGG Gly	ACC Thr	CCA Pro	CAA Gln	CGG Arg 175
TCT	ATG Met 110	ATC Ile	GAT Asp	AGT Ser	GAG Glu
ATT Ile	CAG Gln	TTC Phe 125	TCG Ser	TTC Phe	GAA Glu
CTC Leu	GTT Val	AAT Asn	CTT Leu 140	CCT	CCA Pro
TAC Tyr	$ ext{TGT}$	CAG Gln	GGT Gly	ACT Thr 155	CTT Leu
TGC Cys 90	AAC Asn	GAG Glu	CTG Leu	GAT Asp	AAT Asn 170
AGC Ser	CAG Gln 105	GCG Ala	TTC Phe	GAT Asp	CCC Pro
TCC Ser	GAG Glu	GAA Glu 120	TAC Tyr	ATC Ile	GAA Glu
GGC Gly	AGT Ser	ACT Thr	TCT Ser 135	TGG Trp	CAT His
TTT Phe	ACC Thr	AAT Asn	CTT	CAA Gln 150	CCC
TCA Ser 85	AGC Ser	ATC Ile	TCA Ser	TGG Trp	CAC His 165
AAG Lys	TGG Trp 100	GTG Val	GAG Glu	AAA Lys	TGG Trp
TGG Trp	TTC Phe	GTG Val 115	AAT Asn	GGC	TTC TGG Phe Trp
CAC His	AAC Asn	CTG Leu	CTG Leu 130	AAT Asn	AGG Arg
AAT Asn	GAG Glu	CAT His	CAG Gln	GGT Gly 145	GTC Val

Fig. 40

OGYAKETI OTTODI

754	802	858	918 978 1038 1098 1158 1218
GTT TCA ATA GTT TAC TGG AAT CCT TCG AAA TGG GGC TGG AAT GAT GTT Val Ser Ile Val Tyr Trp Asn Pro Ser Lys Trp Gly Trp Asn Asp Val 180	TTC TGT GAT AGT AAA CAC AAT TCA ATA TGT GAA ATG AAG AAT TAC Phe Cys Asp Ser Lys His Asn Ser Ile Cys Glu Met Lys Lys Ile Tyr 195	CTA TGA GTGCCTGTTA TTCATTAATA TCTTTAAAGT TCAGACCTAC CAAGAAGCCA Leu *	TAACTTCTTG GCCTGTACAT CTGACAGGG CCGTTCTTTT CCTAGCCACT ATTCTTTACT AGAGTCACCT GGGGAGTAGG ATCTTCAGCT AAGGAATTGC CTCTGTCAGC TTGACCAGTC AGCATGTCTG GGGGCATTTT CTTGATTAAT GATTGTTGTA AGAGGGTCCA GGTGGTAAGC AAAGGTGTTA AACCATGAA GAGCAAGCCA GGGAGCATCA TCCATCCATC TCTGCCCTCA TAAGATGAAT AAACAATTTC ATCCAAAAA AAAA

Fig. 4P

OOVERHAL OF LOCA

ω ω ω ω	വവ	നത	3 7	6 5	7 1	പ ന ന ന ന ന ന
6 13 20 27	34	9 N	4 45	50	7 56	628 769 90 90 90
GG GG STT	M Q S H L AACTGCTATCCACAAACACCATTAATCCTTTAGGGAGGCAGAAAAGGCCAGA ATG CAA AGC CAT CTT	GGG	A GCT	V GTT	K AAG	AAA AAA ATA SGG
GTCGACCCACGCGTCCGGAAACCATTCCACAATCACCCTCCTGAGGAACTCTTAGCACTGCATAAAGT GTTCTGAGTTTGTAATCAGATATTGTCACACTGGTTCCTTCAAACAGACATGACAAGGAGCTGGCTTTGG GCTAGGCTGCTCCTTGCCTATGATTGGGGAAGGTTAAACCCCCTACAGGGGCTTATGTATG	H C CAT	S V F L L L W A F I W G G TCT GTC TTT TTA CTT CTC TGG GCC TTT ATC TGG GGA GGG	T W N S E P G Q D S N L W A CT TGG AAC AGT GAG CCT GGC CAG GAC AGT AAC CTG TGG GC	Q CAG	M ATG	K M G E G E I V AAG ATG GGT GAG ATA GTG TAAGACCCTGAGAATGGCATAGGGTAAAACTGGGACAG AGATACTGTGGGAACGAACGATAGCTGCAGAGGGACGAAGGAAG
CTGC2 SCTGC FGGA2 FTGAC	S A AGO	\overline{M}	L	S TCT	T ACA	AACTC SGGAC SGCAA AATTA
AGCAC AGGAC FATGT	G CAZ	I ATC	N AAC	A GCT	EGAG	STAAA SAGAC AATGC STATA
CCTT2 SACA2 FATG1	M A AT(FTTT	S AGT	$_{ m TTA}$	K AAG	ragge agaae raaaz acare sraaz
SAACT ACATO SGCTT	CCAG	A GCC	D GAC	M ATG	E GAG	GGCA: AAGG/ CCAA: CTCA/ ATGG(
rgagc acaga acagc	4AGG(W TGG	Q CAG	R AGG	H CAT	SAAT(AAGG/ SAAC(TATG(SAGA/
CICC: ICAA/ CCCI/	AGAAI	L CIC	299 9	E GAA	R CGA	CTGA(SAGG/ CAAA(AAAA/ IGAT(
CACC	AGGC.	L	P CCT	W TGG	G GGA	GACCO GAGGO AAGAO CATAO ACACO
CAAT(TGGT GGTT/	AGGG.	$_{ m TTA}$	E GAG	E GAA	K AAA	TAA(GACA) TAAG AATA(CTAC)
TCCA(ACAC) GGAA(CACT)	CTLL	F	S AGT	R AGG	E GAG	I V ATA GTG GCAGAGGG ACATTCAT GCCAATAP GATACCAC
CCAT' TGTC' TTGG(AATC	V GTC	N AAC	N AAT	E GAA	I ATA TGCA TACA GGCC AGAT
GAAA ATAT ATGA	CATT	S TCT		S TCT	GGA	E GAG TAGCT ACAAT GAGTG TGTGA
	ACAC	GGG	T ACT	I ATT	GGA	GGG ACGA TCTC TATT GCAC
CGCG GTAA CCTT TAAA	ACAA	L CTA	CCC	I ATT	P CCT	E GAG GAGA AAAC GATA AAAA
CCCA(GITT)	ATCC	T ACA	S TCC	D GAC	C TGT	GGT GGTGG GGAGG AGAT
TCGA(CTGA(AGGC)	IGCI'	F I T L G TTC ATT ACA CTA GGG	H V S P T CAT GTT TCC CCC ACT	C D D I I TGT GAT GAC ATT ATT	L K C P G TTA AAG TGT CCT GGA	K M G E G AAG ATG GGT GAG GGG AGATACTGTGGGAGAACGAT ACAGTTTGGAGAACTCTCA CCACAGAAGATGATATTG AAATGCAAATTAAAAGCACT
GTT(GCT/ GGA/	AAC	$^{ m F}$	H CAT	C TGT	$_{ m L}$	K AAG ACA AAA ACC

Fig. 5A

IGYESETT OTTGOT

GIGAAACCCIGICICTACIAAACAIACAAAAATIAGCIGGGGGGGGGG	1043
ACTCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCCCAGGAGGCAGAGTTACAGTGAGCCGAGATCATGC	1113
CCTTGCACTCTAGCCTGGGTGACAGAGCGAGACTCTGTCTTAAAAAAAA	1183
AAAAAAAAGGGCGGCCGC	1202

Fig. 5B

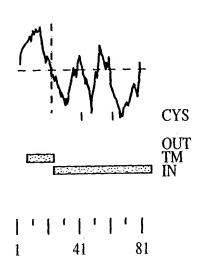


FIG. 5C